

**BIOSYSTEMATIC STUDIES ON THE WHITEFLY *Bemisia tabaci*
(GENNADIUS) (HEMIPTERA: ALEYRODIDAE)**

SHANIKA JAYASEKERA

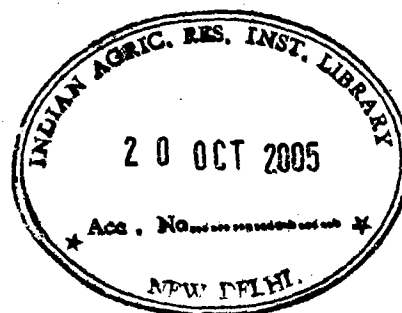
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**DIVISION OF ENTOMOLOGY
INDIAN AGRICULTURAL RESEARCH INSTITUTE
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BIOSYSTEMATIC STUDIES ON THE WHITEFLY *Bemisia tabaci* (GENNADIUS) (HEMIPTERA: ALEYRODIDAE)

by

SHANIKA JAYASEKERA

**A Thesis submitted to the Faculty of Post Graduate School,
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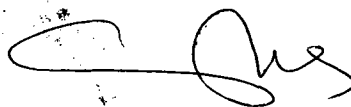
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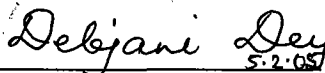
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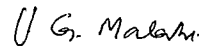
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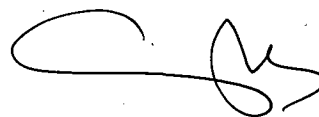
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CERTIFICATE

This is to certify that the thesis entitled "Biosystematic studies on the whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae)", submitted to the Faculty of the Post Graduate School, Indian Agricultural Research Institute, New Delhi, in partial fulfillment of the requirements for the award of the degree of **Doctor of Philosophy in Entomology** by **Ms. Shanika Jayasekera** embodies the results of *bona fide* work carried out by her under my supervision and guidance. No part of the thesis has been submitted by her for any other degree or diploma.

I further certify that any help or information received during the work on this thesis has been duly acknowledged.



(V.V. Ramamurthy)
Chairman
Advisory Committee

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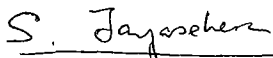
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Introduction

Many insect pests, of which whiteflies are of great significance, affect agriculture, horticulture and forestry worldwide. These are important not only as sucking pests draining out the plant sap, but also more so as vector of many deadly diseases. Their role as vectors is of greater economic importance as even very small populations can spread deadly viruses that can wipe out many important agricultural, horticultural and forest flora. The common name 'whitefly' derives from the presence of secreted powdery wax, which is spruced over the whole body, and wings of adults, invariably of every species. Almost all adult whiteflies possess seven segmented antennae and a fore wing venation that is reduced to a simple or once branched major vein $R+R_s$, with R_1 variably developed. The final whitefly larval stage is usually termed a 'puparium', a name, which reflects the extreme morphological difference between this stage, and the winged adults, whose emergence is facilitated by the rupturing of lines of weakness, which are termed transverse and longitudinal moulting sutures. The vacated puparium is referred to as the pupal case. Most of the whiteflies are usually minute, 1-3 mm long, inconspicuous, and with piercing and sucking mouthparts. Majorities are found infesting the foliage of plants; are all plant feeders, mainly on the phloem tissues. Many species are polyphagous, prolific and highly dispersive.

Whiteflies belong to the order Hemiptera and superfamily Aleyrodoidea, within the suborder Homoptera under Sternorrhyncha. Over 1156 species are known so far from the different geographical regions of the world (Mound and Halsey, 1978). These fall under 126 genera of two subfamilies viz. Aleurodicinae and Aleyrodinae. Morphologically the aleurodids seem to be degenerate psyllids, although ecologically they are the tropical equivalent of aphids. The generic classification of the Aleyrodidae is

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based on the structure of the fourth larval instar, the so called pupal case. Their fecundity and development is host related and extremely sensitive to even slight changes. Normally many of these undergo 11 to 15 generations in a year and can produce as many as 300 eggs per adult. Most species can survive temperatures of -2°C for 80h and has a critical thermal maximum of 52°C .

The reproduction of whiteflies may be either sexual or asexual and in some species unfertilized eggs produce males, but parthenogenetic races of only females are also known. Eggs are attached by short pedicels to the undersurfaces of leaves, frequently arranged in arcs or circles. First instars are flattened, ovoid, with short legs. The second and third instars are sessile, with atrophied legs. The fourth instar (puparium) is similar to the larva but feeds only briefly, and then becomes inactive. On most plants, colonies develop on the undersides of the leaves, a factor that makes diagnosing and managing them very difficult under most of the circumstances. Wax plates or filaments in highly individualized patterns frequently ornament the puparia. Aleurodids are primarily tropical and the economically important species are small in size and have ability to survive transport. Once established these can survive in habitats ranging from temperate through to tropical. This has further allowed many species to increase their distribution through invading new areas of the world. In addition to direct damage to the plant, whiteflies can cause indirect damage through the production of honeydew, which induces sooty mould, and through the transmission of plant viruses. As a result of their waxy covering, high fecundity and stability to develop resistance rapidly, they have proved to be extremely difficult to control through the use of insecticides.

Among the many species of whiteflies, *Bemisia tabaci* (Gennadius) has become an important pest of agricultural and horticultural crops throughout the world. It was first

collected and described from tobacco, *Nicotiana* spp., as *Aleurodes tabaci* by Gennadius in Greece in 1889; and later synonymized by Russell in 1957 into *Bemisia*. It is known by several common names e.g., tobacco whitefly, cotton whitefly, cassava whitefly or sweet potato whitefly. Until recently, the native home of *B. tabaci* was thought to be the Orient, Africa or the Middle East. The present day worldwide distribution of *B. tabaci* has been documented in tropical and subtropical locales on all continents, except in equatorial South America. The first record of occurrence of *B. tabaci* in India was from cotton in 1905 (Misra and Lambda, 1929; Reddy and Rao, 1989), and it became an economic pest of cotton in Punjab by 1919 (Lisha et al., 2003). A survey of literature suggests that score of host plants colonized by *B. tabaci* and the number of hosts has increased over time. Current records indicate that *B. tabaci* can successfully colonize a multitude of host plant species across many families; and devastating losses by both the insect and the viruses, which it transmits, had been reported in particular from India, Pakistan, the Americas and the Caribbean.

Bemisia tabaci is the most important as wide spread vector and only species of whitefly known to transmit viruses of economic importance in India. The vector may retain the virus for periods ranging from two to twenty five days. Some such important diseases transmitted by *B. tabaci* include abutilon mosaic, cassava mosaic, cotton leaf curl, tomato yellow leaf curl, soybean yellow mosaic, sweet potato mild mottle and tobacco leaf curl. The suspicion that *B. tabaci* is a heterogeneous assemblage of genetically different populations has been raised occasionally in the literature since the 1950s. It is based on differences in biological characteristics, host preference, and virus transmission efficiency. The success of *B. tabaci* in its exploitation of a vast range of host plants has generated intensive research efforts during the past few years. The biosystematics of *B. tabaci* is subjected to a lot of controversy recently in India and many

other tropical countries, especially in view of the biotype B (*B. argentifolii*). Banks et al. (2001) reported this biotype B from India, and revealed its role in tomato leaf curl virus disease epidemic. Thus it has been shown that the populations of *B. tabaci* in India are complex and the variations due to the host differences, geographic differences, climatic differences, insecticide pressure differences, and virus transmission differences are enormous.

With the advent of several intraspecific populations as biotypes, identification guides for specified geographical areas become especially important. Morphologically, adults of none of these biotypes have up to now being reliably separated. Bellows *et al* (1994) maintain that while no consistent differences can be found between adults, differences could be found in the 4th instar and pupal case. Comparisons of the differences due to host plants, virus transmission abilities, RAPD and esterase patterns had demonstrated that many biotypes exist. Among these differences, host related phenotypic variations are very important and there had been only few studies on this important aspect (Mound, 1963; Jesudasan *et al.*, 1997; Thompson, 2000; Jayasekera and Ramamurthy, 2003).

It is amply evident that a wider gap exists in our knowledge on phenotypic variations and biotypes of *B. tabaci*, which is required to be tackled, scientifically, especially taxonomically. There is no comprehensive information available on the species diversity, genetic and ecological diversity. These have led to complex situations warranting detailed studies on the morphometric differences, and correlate these with virus transmission and molecular differences. Such studies necessarily envisage scanning the morphology of the puparia as well as adults, evaluation of the different characters and their relationships through morphometrics; standardization of the isolation of genomic DNA, optimization

of PCR in addition to its analysis through molecular studies; evaluate virus vector relationships through transmission studies in the selected populations of *B. tabaci*. With these in mind the present study was undertaken of the populations obtained on brinjal, cotton, okra and soybean from Delhi, with the objectives namely

1. Morphometrics of puparia and the adults
2. Molecular aspects involving PCR of genomic DNA and
3. Virus transmission features

so as to produce consolidated and valid interpretations towards the taxonomic aspects of the intraspecific populations of *B. tabaci*.

Review of Literature

The present study is focused towards the intraspecific populations of *Bemisia tabaci*, on the aspects of morphometric studies of puparia and adults; molecular studies at the genomic DNA level and transmission studies. If one undertakes a review, it will be observed that volumes of literature are available on the different aspects of *B. tabaci*. Such a nearly complete bibliography up to 2001, encompassing all aspects with 997 references is available as Appendix A Bemisia Bibliography at home.zf.jcu.cz/Bemisia.htm. Hence, the review given here is focused towards the relevant aspects of the present study namely host correlated phenotypic/ morphometric studies, molecular variations and virus transmission aspects, only. Even in these the review has been restricted to the population diversity and in case of transmission to only the mungbean yellow mosaic India virus, on which studies have been done now.

2.1. Morphometric studies

From the last larval cast skin or the pupal case of *B. tabaci*, a wide variation in several morphological characters was seen in the populations on the different food plants (David and Ananthakrishnan, 1976). Examples of such intraspecific diversity on six different food plants were discussed showing the type, presence or size of many diagnostic characters. Omran and Khidir (1978) evaluated the preference of *B. tabaci* populations for oviposition in cotton in Sudan. These showed that the whitefly attached its eggs to the base of the leaf hairs. This appears to be the reason for the resistance of smooth-leaved cotton varieties, and for its preference for the hairy-leaved varieties. The cotton varieties previously found resistant to oviposition by *B. tabaci* in free-choice experiments, were compared with the susceptible variety Santa Rosa under no choice conditions and the populations were evaluated (Laurencao and Yuki, 1982).

waxing behaviour. The morphology and lipid composition of wax particles and their application to the body surface of adults were found to be determined by the templates (modified microtrichia) from which they were extruded.

Rajam *et al.*, (1988) studied the influence of host plants on the parasitism of *B. tabaci*. Parasitism was significantly higher on cotton than on lablab, brinjal or the weed prickly chaff. Low rates of parasitism seemed to be associated with greater density of hairs on the leaves and with stoutness of these hairs. Geographic distribution, biology, development, population dynamics, harmfulness, spatial distribution, monitoring and host range, and the role of crop husbandry practices, host plant resistance, associated natural enemies, and insecticides in integrated control, of *B. tabaci* were reviewed by Reddy and Rao (1989). Butler and Vir (1989) evaluated the morphological basis of resistance in cotton to the different populations.

Byrne and Houck (1990) through principal component analysis revealed sexual dimorphism in winged forms of *B. tabaci*; fore- and hind wings of females were larger than those of males. Discriminant function analysis of these indicated subtle morphological differences within the same sex between the wings of migrators and the wings of those engaging only in trivial flight. These differences suggested that *B. tabaci* employs dispersal strategies used by other dimorphic Homoptera that occupy heterogeneous habitats. Glasshouse studies were conducted to determine if there were any differences in rates of oviposition and offspring survival when adults of *B. tabaci* were exposed to two different food plants (Costa *et al.*, 1991).

Bethke *et al.*, (1991) studied the comparative biology, morphometrics, and development of two populations of *B. tabaci* on cotton and poinsettia. Development rates and body sizes of two populations (a 'cotton strain' and a 'poinsettia strain') were observed on both cotton and poinsettia at $25.4 \pm 0.2^{\circ}\text{C}$. There were no significant differences in

female longevity between populations reared on the same host plant or within populations reared on different hosts. Females originating from poinsettia laid significantly more eggs if reared on either poinsettia (85.0 eggs per female) or cotton (51.2 eggs per female) than did females from the cotton population (22.3 eggs per female if reared on poinsettia and 31.8 eggs per female if reared on cotton). Four instars were confirmed using the Brooks-Dyar rule of geometric growth. First to 4th instars from either population had significantly longer body lengths when reared on cotton than those reared on poinsettia. Pupae of the cotton population were longer and wider than pupae of the poinsettia population, and within populations, female pupae were significantly larger than male pupae. Although the tibiae of adult females were longer than those of males, there were no differences between populations within the same sex.

Effects of some morphophysiological characters of leaf on incidence of *B. tabaci* on cotton were studied Ilyas *et al.*, (1991). Specimens were compared to determine the biological and genetic characteristics associated with populations derived from different host plants and geographical locations by Bedford *et al.*, (1992). Several populations could be distinguished by non-specific esterase patterns. Some populations had a broad host range, induced phytotoxic symptoms such as 'silverleaf', had large reproductive capabilities and were efficient vectors of many of the fifteen geminiviruses tested. These populations were referred to as the 'B' biotype. It is concluded that this biotype originated in the Middle East, and is now found throughout the Mediterranean, in South Africa, the Caribbean and Central and North America. Bedford *et al.*, (1994) studied the geminivirus transmission and undertook the biological characterization of the biotypes from different geographic regions. The morphology of the puparia and compound eye structure of adults in addition to wings of adults was analyzed. Setae and spines from the same colony were

found variable depending on host or leaf surface characteristics; however, differences in adult body length were noticed.

Bellows *et al.*, (1994) while describing *B. argentifolii* as a new species from material collected in California and Florida, demonstrated its distinction from *B. tabaci* through crossing experiments, studies on intraspecific and interspecific mating behaviour, analysis of allozymic frequencies, PCR analysis of genomic DNA besides morphological evaluation. The description of the new species was based on morphological characters, namely absence of dorsal seta in the 4th nymphal instar, the width of the thoracic tracheal folds, and the width of the wax extrusions from the tracheal folds. Population phenologies of *B. tabaci* on young cassava crops in Cote d'Ivoire are described for three field seasons during 1988-1990 by Fishpool *et al.*, (1995).

deBarro (1995) reviewed the information on taxonomy, origin, current distribution, host range, ecology, population dynamics, dispersal, damage, viruses transmitted and virus-vector interactions including differences between biotypes A and B. The information on host range was also provided. Morphological and genetic mechanisms associated with the whitefly and tomato plant that may explain observed variations in resistance patterns in *B. argentifolii* were examined (Heinz and Zalom, 1995). Leaf trichome and position relative to the stem terminus were the best predictors of whitefly oviposition rates on tomato cultivars and their wild relatives. Higher oviposition rates occurred on leaves with dense trichomes positioned close to the stem terminus. Leaf trichome density also explained a significant portion of the variance in whitefly oviposition rates among commercial cultivars.

Influence of foliar pubescence on abundance and parasitism of *B. argentifolii* on soybean and groundnut was evaluated by McAuslane *et al.*, (1995). Temperature dependent development, mortality, and adults size of *B. tabaci* biotype B on cotton was

studied by Wagner (1995). The biotype B was reared on 'DES 119' and Pima 'S-6' cotton at 31 constant temperatures. Development times of eggs, nymphs, and the combined immature stages were recorded and assembled into frequency distributions at each temperature. Morphological variation in *Bemisia* endosymbionts was analyzed by Costa *et al.*, (1995). The ultrastructure of the endosymbionts of several populations was examined using transmission electron microscopy. Consistent differences in morphology and relative number of endosymbionts were observed between species and biotypes within *Bemisia*.

Variation in the developmental period of the cotton white fly *B. tabaci* on different host plants, from Tamil Nadu was studied by Ravisankar (1995). First report of B-biotype in Australia was revealed by the studies of Gunning *et al.*, (1995). The insects were identified by esterase isoenzyme patterns. The initial identifications were made in *B. tabaci* collected from a rock melon crop in Darwin, Northern Territory, and from *Euphorbia pulcherrima* in Tamworth, New South Wales. The biotype or host-races concept with respect to *B. tabaci* was reviewed and the worldwide dispersal and impact of the B biotype were discussed (Brown *et al.*, 1995).

Behavioural, morphological, and physiological traits associated with migratory *B. tabaci* were evaluated by Blackmer *et al.*, (1995). Adults that had flown for varying lengths of time (1 min to 2.5 h) in a flight chamber at 28°C were observed to exhibit behavioural, morphological and physiological differences. Oviposition preference of two *Bemisia* species was evaluated as a character by Blua *et al.*, (1995). Adult females of the *B. argentifolii* and *B. tabaci*, were given access to three different host plants in choice and no choice experiments to determine whether oviposition preference could account for field observations of host use. The lowest proportion of eggs laid by *B. argentifolii* was on sugar beet, whereas *B. tabaci* laid its lowest proportion on cabbage. The proportion of

eggs laid on cabbage by *B. argentifolii* was significantly greater than that laid by *B. tabaci*.

Variation in *B. tabaci* populations, based on host plant associations, developmental statistics and growth parameters in Egypt was studied by Gergis and Adam (1996). Monitoring of populations on the basis of thermal and growth parameters on cotton and vegetables revealed a mixture of biotypes on various food plants and at different locations. It is suggested that these populations are of two groups recently derived from the same source. The occurrence of *B. argentifolii* in mid-Egypt was confirmed. Mayer (1996) reviewed the taxonomy, biology, control and management of *B. tabaci*. Polymorphic esterase and acetyl cholinesterase alleles in *B. tabaci* were studied using electrophoretic and colorimetric assays. The segregation of these alleles between parental and F1 generations provided unequivocal evidence of haplodiploidy. Unmated females, heterozygous at a polymorphic locus, produced a 1:1 ratio of haploid males expressing either of the maternal alleles. Although male offspring were produced by both virgin and mated females, the segregation of alleles showed that they were always haploid (homozygous) for the marker enzymes. Females only arose from fertilized eggs and invariably expressed paternal and maternal alleles.

The morphological variations of *B. tabaci* on thirteen species of ornamental plants and one species of vegetable were correlated with the structure of the host leaf (Chen 1997). On hairy leaves, nymphs and pupae were often small with elongated dorsal setae; their margins were crenulated and sometimes indented deeply. On glabrous leaves, they were large with microsetae or least elongated dorsal setae and their margins were smooth. Numerical analyses of host correlated variation in *B. tabaci* were conducted in India, using six different host plants (Jesudasan *et al.*, 1997). The Canberra metric index and distance matrices were calculated. The pupal case of *B. tabaci* from glabrous hosts

showed a small distance index between different host plants and a greater distance index when compared with the pupal cases from nonglabrous hosts. Drost *et al.* (1998) selectively reviewed the life history of *B. tabaci* biotypes in relation to host plants.

The surface lipids of *B. argentifolii* nymphs and exuviae were characterized by Buckner *et al.*, (1999). The identification and distribution of lipids were determined by capillary gas chromatography (CGC) and CGC-mass spectrometry (CGC-MS). The quantity of lipid from exuviae was 80 per cent greater than that from nymphs. The composition for the lipid classes and the chain-length distribution of each lipid class were similar for both nymphs and exuviae. Lipids extracted from the exuviae from laboratory-reared sweet potato whiteflies, *B. tabaci*, were essentially the same as the lipids from *B. argentifolii*.

A study examined the relationships between cotton leaf morphology and *B. tabaci* population densities in eight United States Deltapine and six Australian cotton cultivars and breeding lines at Holtville, California (Chu *et al.*, 1999). Results showed that okra leaf cultivars and lines were colonised with fewer whitefly adults, eggs and nymphs compared to normal-leaf cultivars. The distance from under leaf surfaces of cotton leaves to the centres of nearest minor vascular bundles was negatively correlated with whitefly adult, egg and nymphal densities on leaves for all genotypes with the exception of the Australian breeding line 89013-114. The results suggest that okra-leaf and distance from under leaf surfaces to the centre of nearest minor vascular bundles of cotton leaves are genetic traits that have potential for breeding whitefly-resistant upland cotton cultivars.

Lee *et al.*, (2000) studied the morphological characteristics of *B. tabaci* by scanning electron microscopy and described the same comparing them with *Trialeurodes vaporariorum* (Westwood). This study included the comparison of morphological characters of *B. tabaci* with those of DNA markers. The biotype identity in Korea was

thus determined by morphological studies in unison with molecular studies. Benmessaoud *et al.* (2000) analysed the wax secretions in *B. tabaci* in Algeria and its evolution during the larval development cycle. Thompson (2000) studied the development, morphometrics and other biological characteristics of *B. tabaci* on cassava in Guyana and a description of the different nymphal instars and other biological characteristics was made. Regression analysis was highly significant between the length and width of nymphal instars modelled collectively, indicating two-dimensional growth at least across three nymphal stadia. Males were smaller than females on the basis of body length, wing width and width of the abdomen.

The variation in the *B. tabaci* complex in the USA was studied by Kirk *et al.* (2000). Collections from Thailand grouped separately from B types from Arizona and Florida, and the target B type from Texas, USA, a cluster from India, and other New World populations. The Spanish *B. tabaci* was found to be most closely related to non-B type populations from Spain and Sudan. For evaluating their variations host parasitoid relationships were deployed. *B. tabaci* B biotype was first reported in India and it was associated with tomato leaf curl virus disease epidemic (Banks *et al.*, 1998). Ghahari and Hatami (2001) investigated the morphological and biological characteristics of six species of whiteflies from Iran, and this study included *B. tabaci*, *B. argentifolii*, and *B. hancoki*. Morphological characteristics and different growth stages of including egg, first to fourth nymphal instars and adults were defined and figured. Quintero *et al.* (1998) evaluated the relationships between species and biotypes of whiteflies affecting annual crops in Colombia and Ecuador. Attique *et al.* (2001) studied the host preference of *B. tabaci* for oviposition, developmental period and survival, through multiple choice tests in field cages. 23 plant species including three crops, three fruit and forest plants, five ornamental plants and twelve weeds were compared for their preference for oviposition and

development. Studies on the stylet penetration by *B. argentifolii* on the host leaf surface and its morphology led to significant findings (Freeman *et al.*, 2001).

Gerling (2002) conducted studies on whiteflies in Israel and produced new information on fitness enhancing characteristics. The wax that the ovipositing whitefly mothers deposit, the flocculent wax or spines adorning the nymphs, especially those growing on pubescent leaves and the exuviae of early nymphal instar that may remain upon the later ones, were all shown to serve as fitness related functions by enhancing competitive ability or, more often, protecting against natural enemies. The appearance of these biotypes was related to the very large populations that developed, their vast ranges and host plant varieties, to various selective pressures and to the physiological characteristics of the species.

Gocmen and Devran (2002) studied genetic variation of *B. tabaci* populations, collected from tomato, cotton, cucumber, brinjal, and peppermint, in Antalya and Turkey. The similarity values obtained through amplified fragment length polymorphism were related with morphological studies for logical conclusions. Experiments were conducted at Ludhiana in Punjab to determine the relative preference of *B. tabaci* to nine different host plants (Aneja *et al.*, 2002). Lisha *et al.* (2003) evaluated the host plant performance, esterase and virus transmission aspects of cassava and sweet potato strains. A pilot study was done on the host related phenotypic variations in *B. tabaci* on cotton, soybean and *Hibiscus rosa sinensis*. It was reported that variations in terms of length, breadth and number of dorsal setae of the puparia due to hosts is a natural and common phenomenon (Jayasekera and Ramamurthy, 2003).

2.2. Molecular Studies

Polyacrylamide gel electrophoresis was used to compare non-specific esterase isoenzymes in adults of the whitefly species *B. tabaci*, *Trialeurodes abutiloneus* and *T.*

vaporariorum. (Prabhaker *et al.*, 1987). Based on the mobilities of the isoenzyme, the esterase loci could be used to differentiate the species. Specimens of *B. tabaci* were compared to determine the biological and genetic characteristics associated with populations derived from different host plants and geographical locations by Bedford *et al.*, (1992). Several populations could be distinguished by non-specific esterase patterns. RAPD-PCR was used to demonstrate DNA differences between the A and B biotypes of *B. tabaci* (Gawel and Bartlett, 1993); all twenty of the RAPD primers tested distinguished readily between the biotypes. DNA extracted from individual eggs and nymphs showed identical differences. RAPD-based genetic similarity statistics indicate that the two biotypes were no more similar to each other. It was concluded that RAPD-PCR may be useful in distinguishing closely related organisms.

Considerable and significant heterogeneity in esterase allele frequencies was found among samples of *B. tabaci* collected from different hosts and localities in Israel (Wool *et al.*, 1993). The B biotype was found to be characterized by a diagnostic esterase-banding pattern (Bedford *et al.*, 1994). Bellows *et al.* (1994) while describing *B. argentifolii* as a new species demonstrated its distinction through analysis of allozymic frequencies and PCR analysis of genomic DNA, in addition to morphological evaluation. Jimenez *et al.* (1994) conducted a study to evaluate whether the double-stranded RNA (dsRNA) occurred in geographically remote populations of the biotypes.

Significant heterogeneity in esterase allele frequencies was found among samples of *B. tabaci* collected from different food plants and localities in Colombia by Wool *et al.* (1994). Biochemical properties of the predominant esterases found in the two distinct populations, considered to be different biotypes of *B. tabaci*, were investigated by Coats *et al.* (1994). General esterases, previously established as diagnostic markers on native PAGE for the 'A' and 'B' biotypes, were characterized with respect to molecular masses,

isoelectric points, isomeric relationships and substrate specificities. Lisha *et al.* (2003) used PCR based molecular diagnostics; Single stranded conformational polymorphism analysis revealed a remarkable lack of nucleotide variation among strains conforming to the B biotype, whereas several of the non-B strains exhibited different banding patterns.

First report of B-biotype of *B. tabaci* in Australia was revealed by the studies of Gunning *et al.* (1995), through studies on the esterase isoenzyme patterns. Brown *et al.* (1995) reviewed the worldwide dispersal and impact of the B biotype on agriculture, molecular and biochemical aspects. Polymorphic esterase and acetyl cholinesterase alleles in *B. tabaci* were studied using electrophoretic and colorimetric assays (Byrne *et al.*, 1996). deBarro and Driver (1997) described the use of PCR to identify the B biotype and distinguish it from other biotypes and species of whitefly. Guirao *et al.* (1997) surveyed the biotype status of the Spanish populations of *B. tabaci*, and this study involved observation of squash silverleaf reaction, analysis of esterase patterns and application of PCR.

PCR was used to identify samples of adults of *B. tabaci* from Africa and Central America, collected on different host plants (Menozzi, 1997). Analysis of the amplification patterns using the UPGMA method revealed the existence of several biotypes, which varied according to the food plant and the geographical location. deBarro *et al.* (1998) discussed the distribution and identity of biotypes from eighteen pacific countries. The presence of biotype B was confirmed in Colombia through biochemical, molecular and etiological tests by Quintero *et al.*, (1998). At the molecular level, RAPD amplification products obtained with the primers OPA-04, OPA-11 and OPA-17 were also found to be different between biotypes A and B. Loxdale and Lushai (1998) reviewed the use of molecular markers in entomology and highlighted the use of PCR in differentiating the intraspecific populations.

A phylogeographical analysis of the *B. tabaci* species complex based on mitochondrial DNA markers was undertaken by Frohlich *et al.* (1999). These data confirmed the biochemical, genetic and behavioural polymorphisms described previously for *B. tabaci*. The consideration of all global variants of *B. tabaci* as a highly cryptic group of sibling species was argued. Twenty-one whitefly populations in the genus *Bemisia* were evaluated for genetic variation at three allozyme loci (Brown, 2000). Nine of the 22 populations that exhibited polymorphic loci were subjected to allozyme analysis using a minimum of 10 enzymes, representing 10 to 14 distinct loci. Among those nine variants examined, calculated genetic distances ranged between 0.03 and 0.52, with three main groups emerging from the analysis. Caterino *et al.* (2000) discussed the current state of insect molecular systematics to highlight the markers, which can be deployed at the different taxonomic levels.

deOliveira *et al.* (2000) used RAPD analysis to evaluate the genetic variability of 12 Brazilian populations of *Bemisia* spp. Ten primers were analysed in order to detect polymorphism between samples. The results showed that individuals from a colony maintained since 1983 had similar patterns of *B. tabaci* originated from California, USA. The other samples showed similar patterns to *B. tabaci* biotype B (= *B. argentifolii*), also from California, USA, indicating a great dissemination of this biotype in Brazil. Phenetic analysis of populations revealed high homogeneity between individuals of the B biotype. The genetic structure of six Iberian populations of the whitefly *B. tabaci*, using PCR was investigated by Moya *et al.* (2000). A total of 336 individuals were completely discriminated by means of 234 scored bands. Separate analyses of molecular variance of haploid males and diploid females using the pair wise number of differences between haplotypes showed that biotypes contribute significantly more to the observed variability than populations within biotypes.

Lee *et al.* (2000) included the comparison of morphological characters with those of DNA markers including PCR of DNA and restriction fragment length polymorphism of mitochondrial 12S and 16S rRNA genes, for the identity of biotypes of *B. tabaci* in Korea. The correct identification of *B. tabaci* was observed to be problematic since it was highly polymorphic with extreme plasticity in key morphological characters that vary according to the host, hence RAPD-PCR was used to survey the B biotype and other biotypes in Brazil (Lima *et al.*, 2000).

deBarro *et al.* (2000) evaluated the phylogenetic relationships of world populations of *B. tabaci* using ribosomal ITS1. ITS1-rDNA sequences were analysed to assess the phylogenies among 31 populations. Genetic similarities between 13 samples belonging to nine reference biotypes and two field populations of *B. tabaci* were studied by Cervera *et al.* (2000). These results were consistent with a previous grouping of biotypes based on RAPD-PCR analysis. Identification and molecular classification of *B. tabaci* associated with parasitoid collections and in the release site in Texas were accomplished using morphological traits and nucleotide sequence comparison of the mitochondrial cytochrome oxidase I gene (COI) (700-720 bp) (Kirk *et al.*, 2000).

Calvert *et al.* (2000) undertook morphological and mitochondrial DNA marker analyses of whiteflies colonizing cassava and beans in Colombia. RAPD markers proved complementary to the morphological identification of whitefly species. From each species of whitefly, a region of the mitochondrial 16S rDNA gene was amplified, cloned and the sequence determined. Parsimony and distance analyses were performed and the results were similar to those based on morphology. The relationships between species and biotypes of whiteflies affecting annual crops in Colombia and Ecuador were evaluated by Quintero *et al.* (1998). Biotypes A and B were identified through PCR of DNA with the primer OPA-04.

Maruthi *et al.* (2001) attempted to determine whether a novel *B. tabaci* biotype was associated with the CMVD pandemic utilizing RAPD. The use of these markers for detection of possible selective pressures in *B. tabaci* was evaluated by Callejas *et al.*, (2001). Their results demonstrate that RAPD markers could be useful for the study of evolutionary processes, as well as population genetic structure and taxonomy studies. Gocmen and Devran (2002) studied genetic variation of eight *B. tabaci* populations, collected from tomato, cotton, cucumber, brinjal, and peppermint, in Antalya and Turkey. Analysis of *B. tabaci* population with 11 amplified fragment length polymorphism primer pairs identified a total of 547 fragments, of which 389 were polymorphic. Molecular evidence for the occurrence of two cassava colonizing *B. tabaci* genotype clusters was presented by Legg *et al.* (2002).

Ten populations collected from eight field and ornamental crops from seven provinces/cities in China, were determined using PCR. Results showed that the populations could be classified into three distinct groups: a Biotype B group, a Guangxi group, and a Fujian group (Wu *et al.*, 2002). The biotype status of samples of *B. tabaci* collected from several field and greenhouse sites in Israel during 1999-2000, was determined by polyacrylamide gel electrophoresis (PAGE) for general esterases and by PCR using primers of arbitrary sequence (Horowitz *et al.*, 2003). The results of this survey provide the first published evidence for the occurrence of *B. tabaci* Q biotype, alongside the more widely distributed B biotype.

Twenty-three populations from 23 different cities of 14 provinces in China were identified and differentiated using RAPD-PCR with a primer H16 (Qiu *et al.*, 2003). The results showed that 17 whitefly specimens from 11 provinces were of the B biotype. Comparison of mitochondrial cytochrome oxidase I gene sequences for the populations from Argentina and Bolivia and these were evaluated for their divergence (Viscarret *et al.*,

2003). Lisha *et al.* (2003) evaluated the sweet potato and cassava strains of *B. tabaci* through esterase banding patterns. Abdullahi *et al.* (2004) used RFLP analysis of the ribosomal DNA internal transcribed spacer regions to distinguish cassava-associated populations from other host-associated populations. Endonuclease restriction profile analysis indicated that cassava associated populations from Africa represent a distinct group, with a significant level of separation into subgroups that were not linked to geographical origin. Berry *et al.* (2004) undertook a phylogenetic analysis of *B. tabaci* mtCOI. Haplotypes examined thus far from the African continent had revealed five major cassava-associated haplotypes, which grouped primarily based on extant geography.

2.3. Transmission studies

Bird *et al.* (1973) concluded that golden yellow mosaic of beans is transmitted by *B. tabaci*, and showed that the virus could be retained in the vector for up to six days. Transmission rates were low when the acquisition or inoculation feeds were of short duration, but most of the test plants became infected when the feeds lasted 24 h. The rate of transmission was positively correlated with the number of whiteflies per test plant. Virus-vector relationships of mung bean yellow mosaic virus were studied by Nair and Nene (1973). Virus acquisition and inoculation feeding by *B. tabaci* required a minimum period of 15 min. each. Starvation, particularly before acquisition, increased transmission efficiency. The incubation period in the vector was >3 h. Disease expression was the same irrespective of the number of vectors. The vector retained the virus until its death (10 days) but transmission decreased with period of retention.

During a survey conducted by Suteri (1974), in 1971-72 of the virus diseases of soybean in Uttar Pradesh, plants affected by yellow mosaic virus were found in all areas except the hill regions, the incidence being 20-40 per cent according to the locality. Studies on transmission showed that it could be possible only with *B. tabaci* as vector. A

preacquisition fast of 6h, an acquisition-feeding period of 2h and an inoculation-feeding period of 24h resulted in 60 per cent infection of soybean plants. Rath and Nene (1974) studies in relation to the transmission of mung bean yellow mosaic virus showed that females were thrice more efficient than males as vectors.

Muniyappa *et al.* (1975) reported that a yellow mosaic disease was found affecting horse gram on a farm at Bangalore, Karnataka. When groups of five field-collected adults of *B. tabaci* that had been allowed acquisition feeds of two days on infected plants were confined for two days on healthy seedlings, all the test plants became infected, symptoms appearing in 7-12 days. Verma *et al.* (1975) showed that a single whitefly is capable of transmission of mosaic virus in tomato. The latent period of the virus in the vector was observed to be between 21 and 24 h. The virus can be acquired by the vector throughout the year and retained in the insect. Costa (1976) reviewed all aspects of whitefly transmitted plant viruses and gave a comprehensive account of virus vector relationships.

Rath and Nene (1976) investigated the influence of different host combinations on virus-vector relation of mungbean yellow mosaic virus. The minimum acquisition and inoculation periods required for *B. tabaci* to become infective were 15->60 min and 10->60 min, respectively. The adults required longer acquisition and inoculation periods to infect Bragg soybean and T21 pigeon pea than *Phaseolus mungo* and *P. aureus*. Muniyappa and Reddy (1976) studied the virus vector relationships of the yellow mosaic disease of horse gram. The results showed that the plastic tube method for virus transmission was suitable for whiteflies with slight modifications. Minimum acquisition feeding period was found to be 30 min. but the vector required another 6 h to become viruliferous. Minimum inoculation feeding period was 10 min. The whiteflies remained infective for up to 12 days.

Ahmad (1978) surveyed cowpea in the plains of Punjab Province, Pakistan, in 1972 to 1975 and showed that a yellow mosaic disease, presumably caused by a virus, was widespread. Tests showed that the causal agent is transmissible by grafting and by *B. tabaci* but not through sap, seed, dodder or soil. The disease appeared to be distinct from the yellow mosaic disease of urd and mung beans. Muniyappa *et al.* (1978) studied the epidemiology of yellow mosaic disease of horse gram. Their results showed that disease incidence was closely related to the size of vector populations of *B. tabaci*.

Adults of *B. tabaci*, collected in the field in India, in groups of 5, each acquired soybean yellow mosaic virus within 17 min. and transmitted it during 16 min. inoculation feeding. Adults from colonies reared on tomato and soybean caused a minimum of 53 per cent and a maximum of 87 per cent transmission of the virus. Pre-acquisition and pre-inoculation starving of the insects did not influence transmission efficiency. Virus transmission was only 7 per cent on the cotyledonary-inoculated leaves of the test soybean plants, increasing to 37 per cent when the viruliferous whiteflies were fed on the first trifoliate leaf for 24 h. A higher rate of virus transmission was obtained with a younger virus source (1 month); increased abundance of whiteflies from 1 to 50/plant increased the rate of virus transmission from 23 to 83 per cent (Gill and Rataul, 1978).

Rao *et al.* (1980) studied the yellow mosaic virus observed on groundnut at Hyderabad in Andhra Pradesh. The disease proved to be transmissible by grafting and also by *B. tabaci*, which acquired the virus from diseased plants in 2 days and (at the rate of 15 insects/plant) were able to transmit it in 2 days to *Vigna radiata*, *V. mungo*, *Lablab purpureus*, *Dolichos biflorus* and *Cajanus cajan*, all of which reacted with bright yellow mosaic. Chenulu *et al.* (1980) concluded that primary and first trifoliate leaves of *V. radiata* were suitable for transmission of mung bean yellow mosaic virus by *B. tabaci*. Transmission was found to be influenced by acquisition and transmission feeding times,

number of insects/plant and plant susceptibility. A 5-6 h latent period, after 1 h acquisition feeding, was observed to be necessary.

The weed *Micrococca mercurialis* was found with yellow mosaic symptoms in a survey of virus diseases of plants in Kerala (Mathew *et al.*, 1982). The minimum number of individual aleyrodids needed for successful transmission was found to be two in this case. The virus did not produce any discernible symptoms when inoculated into 50 different plants belonging to 12 families. The virus had a dilution end point of 1:10-1:25, a thermal inactivation point of 50-55°C and an in vitro lifespan of 8-16 h at 27-32°C and 24-32 h at 5-10°C. Bos (1986) discussed the ecology of plant viruses and drew attention on the *B. tabaci* on soybean in Brazil, which led to markedly increased transmission of golden yellow mosaic virus.

In transmission experiments, Verma *et al.* (1989) had reported that the differential transmissibility of yellow mosaic virus diseases on *Vigna radiata*, *Vigna mungo* and *Lablab purpureus* to different hosts was not due to biological differences in whiteflies but due to host-virus-vector interactions. Varma *et al.* (1992) reviewed the symptoms, host range, structural and biochemical changes in the host, particle morphology, serological relationships and nucleic acid spot hybridization, virus vector relations, ecology of the vector and MYMV transmission and control in India. The efficiency of *B. tabaci*, in the transmission of mungbean yellow mosaic virus in different source-test plant combinations was investigated by Dhingra and Ghosh (1993). This investigation showed that virus transmission increased with the number of adult whiteflies/test plant. Nymphs were less efficient vectors than adults when the tests were conducted within the same plant species. Markham *et al.* (1994) reviewed the transmission of geminiviruses by *B. tabaci* and highlighted the emergence of polyphagous B biotype with its increased host range. Fifteen

whitefly transmitted geminiviruses from different geographic regions were evaluated for their transmission characteristics (Bedford *et al.*, 1994)

Systemic infection of *Vigna mungo* using the cloned DNAs of the black gram isolate of mungbean yellow mosaic geminivirus through agroinoculation and transmission of the progeny virus by whiteflies was studied by Mandal *et al.* (1997). The results showed that agroinfected plants contained different forms of DNA characteristic of whitefly-transmitted geminiviruses, and the virus from agroinfected plants was transmissible by *B. tabaci*. The causal virus of yellow mosaic of pigeon pea was found to be an extended host range phenotype of mung bean yellow mosaic bigeminivirus (MYMV) (Mandal *et al.*, 1998). The pigeon pea isolate (MYMV-Pp) was transmitted by *B. tabaci* to mung beans, black gram, French bean, soybean, lima beans, horse gram and cowpeas. Keshwal *et al.* (1999) studied the yellow mosaic disease of soybean caused by soybean yellow mosaic virus in Jabalpur, Madhya Pradesh. Out of thirteen weed and wild hosts recorded under natural conditions, four were confirmed by *B. tabaci* transmission tests to harbour the disease as well as the vector. Rossell *et al.* (1999) traced the transmission pathway through PCR in whitefly extracts and their tissue products after the acquisition access periods ranging from 0.5 to 96h on virus infected plants.

Material and Methods

3.1. Morphometric studies

3.1.1. Material

Morphometric studies were carried out on the intraspecific populations of *Bemisia tabaci* on the selected crops viz. cotton (cultivar Pusa 8-6), soybean (cultivar Pusa 16), brinjal (cultivar Pusa hybrid 5) and okra (cultivar Pusa 4). The studies were conducted on the puparia as well as the adults, which formed the material for the study.

3.1.2. Methods

3.1.2.1. Morphometrics of puparia

a. Collection, preparation and preservation

Collections were made from the research farms of Indian Agricultural Research Institute (IARI) from the four selected crops during July to December; from soybean and cotton in July and from okra and brinjal in September and December, respectively with the help of a field lens (20x). A sample of about 100 puparia was collected from each crop. The collections were made on the same day or on consecutive days in order to maintain homogeneity of samples. Whenever puparia were located on the undersurface of the leaf, leaf samples were carefully plucked, placed in a polythene cover and brought to the laboratory. Each leaf sample was examined under the Wild M8 stereo zoom microscope at magnifications of 6x to 50x with the help of incident light illuminators. Intact puparia were carefully removed from the undersurface of the leaf with the help of an entomological needle. They were then immediately placed in micro vials containing ethyl alcohol. Enough care was taken to label these specimens with data like host, date of collection, locality and details of collector.

b. Selection of samples

The puparia collected were individually examined under Leitz Ortholux II compound microscope at a magnification of 50x to 500x to confirm uniformity and suitability for morphometric analyses. The physical condition like cleanliness, completeness, and amenability for measurement were the criteria utilized here for selection of specimens. Such good puparia of nearly uniform and stable conditions with least variability were randomly selected to have 50 puparia for each of the intraspecific populations. These selected puparia were individually numbered and stored in micro vials with ethyl alcohol before undertaking morphometric analyses. Then using a fine entomological needle puparia were transferred to cavity blocks containing 1:1 glycerol and ethyl alcohol. Each cavity block was labeled with details of host, date of collection, locality and collector's name.

c. Selection of characters

The available taxonomic literature on the descriptions/ redescriptions of *B. tabaci* and its diagnostics at different hierarchical levels were consulted for this task. Studies by Maskell (1895), Cockerell (1902), Bemis (1904), Singh (1931), Takahashi (1954), Mound (1963; 1966), Mound and Halsey (1978), Jesudasan and David (1991) and Martin et al., (2000) on the taxonomy and morphometrics in whiteflies were taken into consideration. A total of 77 characters were considered which were crucial in defining *B. tabaci* at all its taxonomical levels (Table 1 and Fig. 10). In this process, the criteria proposed by Sneath and Soakal (1973) and the basic theories, as detailed by Zelditch et al. (2004) in the book entitled "Geometric morphometrics for biologists: a primer" were taken into account. A preliminary trial was carried out taking 20 puparia of each sample for standardization of characters and to sort out the characters. Those characters that were not found uniformly either on the specimens collected from same host or characters that were not uniform in

different hosts were then eliminated. Literature indicates that puparia are of extreme importance in identification of *B. tabaci*, and hence all characters available on puparia and used for identification were taken into consideration. It was observed that characters like dorsal setae vary even within the same leaf or characters like legs, transverse suture, dorsal papillae, thoracic tracheal comb and fold, which had been used variously by taxonomists were not included due to the reason that these were inconsistent and not amenable for measurement. Thus 39 characters were selected for morphometric studies on puparia (Table 1; Fig. 1-6).

d. Study and measurement of characters

The individual puparia were studied carefully under the research microscope for the selected measurements. While studying so, care was taken to ensure that the puparia are always in a level plane or set uniformly every time in the same angle. To standardize these, initially a trial run was made with five puparia each for every measurement chosen and the standardization was made at that plane and angle that ensured uniformity and concordant values. While doing so, the precautions to be taken at the time of microscopic examinations of taxonomic characters by different workers were kept in mind. The puparia were first analyzed and confirmed for the specific characters of *B. tabaci* before proceeding with the measurements of the selected characters. Then these puparia were individually examined for their morphometrics utilizing Leitz Ortholux II compound microscope at magnifications of 50x-500x fitted with ocular micrometer. The magnifications at which different measurements were taken are indicated in the respective tables. The measurements in terms of ocular values thus tabulated were further subjected to statistical analyses. Such analyses were also undertaken in selected cases on the ratios of different measurements. In case of puparia these include length vs. breadth at middle,

length vs. breadth of abdominal segments 1 to 8 individually, length vs. breadth at middle of caudal furrow and length vs. breadth at middle of vasiform orifice.

3.1.2.2. Morphometrics of adults

a. Collection, preparation and preservation

Collections were made from the research farms of Indian Agricultural Research Institute (IARI) from the four selected crops during July to December; from soybean and cotton in July and from okra and brinjal in September and December, respectively. A sample of about 100 specimens was collected from each crop using an aspirator. The collections were made on the same day or on consecutive days in order to maintain homogeneity of samples. Enough care was taken to label these specimens with data like host name, date of collection, locality and details of collector before suitably storing. The specimens collected were initially examined under the Wild M8 stereo zoom microscope at magnifications of 6x to 50x for completeness and intact conditions suitable for morphometric analyses. The specimens were transferred alive to ethyl alcohol after removing from the aspirator using a fine brush and needle into cavity blocks containing 1:1 glycerol and ethyl alcohol. Each cavity block was labeled with details of host, date of collection, locality and collector's name.

b. Selection of samples

These collected specimens were individually examined under Leitz Ortholux II compound microscope at magnifications of 40x to 100x to confirm uniformity and suitability for morphometrics. The physical condition like cleanliness, completeness, and amenability for measurement were the criteria utilized here for selection of specimens. Such good specimens of nearly uniform and stable conditions with least variability were randomly selected to have 50 specimens for each of the intraspecific populations. These selected specimens were individually numbered and stored in micro vials with ethyl

alcohol before undertaking morphometric analyses. Due attention was paid to maintain the details of host name, date of collection, locality and details of collector on the selected specimens.

c. Selection of characters

The perusal of available taxonomic literature and the taxonomic characters indicated that adults are not taxonomically important and valid taxonomic characters are not available in adults. Hence, simple measurements in terms of length and breadth of different antennal segments, proboscis, head, compound eyes, thorax and abdomen were initially done on trial basis and irrelevant characters were culled out. Due care was taken to avoid any bias in the selection of these characters. While selecting these characters the criteria proposed by Sneath and Soakal (1973) and the basic theories, as detailed by Zelditch *et al.* (2004) in the book entitled “Geometric morphometrics for biologists: a primer” were taken into account. Thus out of the 24 measurements taken, the morphometric analyses of the adults narrowed down to ten characters, namely length and breadth of proboscis, head, compound eyes, thorax and abdomen (Table 2; Fig. 7).

d. Study and measurement of characters

The individual specimens were studied carefully under the research microscope for the selected measurements. While studying so, care was taken to ensure that the specimens are always in a level plane or set uniformly every time in the same angle. To standardize these, initially a trial run was made with five specimens each for every measurement chosen and the standardization was made at that plane and angle that ensured uniformity and concordant values. While doing so, the precautions to be taken at the time of microscopic examinations of taxonomic characters by different workers were kept in mind. The specimens were first analyzed and confirmed for the specific characters of *B. tabaci* before proceeding with the measurements of the selected characters. The

specimens were individually examined for their morphometrics utilizing Leitz Ortholux II compound microscope at magnifications of 50x-500x fitted with ocular micrometer. The magnifications at which different measurements were taken are indicated in the respective tables. The measurements in terms of ocular values thus tabulated were further subjected to statistical analyses. Such analyses were also undertaken in selected cases on the ratios of different measurements. In case of adults these include length vs. breadth of head, compound eye, proboscis, thorax and that of abdomen as a whole.

3.1.2.3. Statistical analysis

The measurements of the taxonomic characters of puparia and adults were tabulated separately for the different populations. In spite of the best efforts, due to improper orientation of specimens and due to damage to specimens while handling, in some specimens, one or more taxonomic characters could not be observed and these were taken as missing entries for statistical analyses purposes. Before entering a measurement in a table, it was ensured that uniformity, objectivity, unbiased ness and conformity are all adhered to, with an objective of reducing errors. The table for each of the characters for the samples from different populations was thus prepared finally for statistical analyses.

The missing values in the tables of character matrices were handled differently depending on the type of analysis performed. For computing simple statistics such as mean, variance, one way single factor analysis of variance (ANOVA), t tests by least square difference (LSD), coefficient of variation (CV) and simple correlation coefficients which permit unequal number of replications, the missing values were removed before the analyses. However, for multivariate techniques, where all the characters were taken at the same time, even if there is one missing value, the entire sample or the variable was omitted. This was accomplished in some cases by imputing the mean values for a variable in place of missing values. However, in all cases it was ensured that the optimum

sample size essential for the different statistical analyses was maintained and the number of imputed values does not exceed 1 per cent, so that these do not seriously impede the results and interpretation.

To statistically analyze the recorded data, MS Windows (version 2000) operated MS Excel (version 2000) or SAS version 8.1 loaded in a PC with Intel Pentium 4 processor was utilized. The main objective of the statistical analysis is to know whether the variation in a character, between the individuals of a sample of a population is significant or not, and whether these populations vary from each other, with respect to their taxonomic characters. Hence, with this in mind, following statistical analyses were conducted.

i. One-way single factor Analysis of Variance (ANOVA): The single factor ANOVA results in terms of variance were evaluated for their significance using F-values, at probability levels of 0.05 and 0.01 and their significance taken into account for interpretations on morphometrics.

ii. Coefficient of variation (CV): To evaluate the stability and consistency of a character and to assess the utility of a character for its diagnostic value the coefficient of variation analyses were done for each character.

iii. Simple correlation studies: To know the kind and extent of relationship between the taxonomic characters, simple correlation coefficients (r values) were worked out considering the different populations separately and as a whole.

iv. Least Square Differences of Means: The means of the different characters in the populations were analyzed and the least square difference calculated to indicate the level of significance in their differences.

v. Multivariate analyses: These analyses included

- **Multivariate Analysis of Variance (MANOVA):** This analysis was used to find out the significant variations between the four populations by way of subjecting all the study characters combined. The significant characters that were found out using single factor ANOVA were taken together and tested using MANOVA. If MANOVA showed significant difference between the populations from different crops, further multivariate techniques like Principal Component Analysis (PCA) and Discriminant Function Analysis (DFA) could be used. In the multivariate analyses of puparia, the 34 characters and in case of adults, the eight characters that showed statistically significant variations in the one-way single factor ANOVA were included. The statistically non significant characters namely ABB6, ABB7, LB3, VO1 and VOB4 of puparia and CEB and PB1 of adults were excluded.
- **Principal Component Analysis (PCA):** This is a statistical procedure to reduce the number of variables by projecting the original measured variables into a new set of variables that has some inherent statistical properties. This analysis is thus used to investigate morphological variations and thereby exploring differences among the groups by effectively reducing the dimension of the problem. In simple terms, the principal components are nothing but linear combinations of original variables, which have special properties in terms of variances. For example, the first principal component is the normalized linear combination (the sum of squares of the coefficients being one) with maximum variance. Moreover, the principal components are generated in such a way that the second principal component is orthogonal to the first component and has second highest variance. Similarly, other principal components are generated. Thus, the principal components are

arranged automatically in descending order of variance. The total number of principal components that could be generated is the total number of measurements considered. Since the number of measurements is very high, using the principal component analysis, it is possible to select first few principal components, which have large variations and could explain the differences in the populations. The principal components can also be used to see whether there are any differences between the populations through plotting the observations in principal component axis.

- **Discriminant Function Analysis (DFA):** This is used to assess the utility of the study characters and for separating the populations in question. In other words it determines whether the characters are able to discriminate between the different populations. Since, there are four populations, there would be three discriminant functions. Using the discriminant functions, it is possible to classify the observations. Some cases may be incorrectly classified and the error rate estimates can also be obtained. Since the same data set was used to develop the discriminant function as well as for estimating the error, the estimates may not be reliable. To obtain reliable misclassification error estimate, the classifications of an individual case was made by excluding the observation from the analysis and computing new discriminant function and classifying the excluded case. This method commonly known as Jackknifed discriminant function was used to estimate the reclassification error rates.

3.2. Molecular studies

a. Collection, preparation and preservation of samples

Collections were made from the research farms of Indian Agricultural Research Institute (IARI) from the four selected crops during July to December; from soybean and

cotton in July and from okra and brinjal in September and December, respectively. A sample of about 100 adults was collected from each crop using an aspirator. The collections were made on the same day or on consecutive days in order to maintain homogeneity of samples. Enough care was taken to label these specimens with data like host name, date of collection, locality and details of collector before suitably storing when alive in micro vials with absolute alcohol.

Essential protocols of sterilization of buffers, glass wares and plastics and other molecular biological techniques followed were as given in Sambrook and Russel (2001). The composition of buffers, general solutions and molecular weight markers are as follows:

Composition of buffers, general solutions and molecular weight marker

CTAB buffer	Modified CTAB DNA Extraction buffer (DEB)- 10ml	Lysis buffer
1.5M NaCl 100 M Tris-Cl pH 8.0 10mM EDTA pH 8.0 2% CTAB 0.1%β mercaptoethanol	1M Tris-Cl pH 8.0 0.5M EDTA 5 M NaCl 10% CTAB 0.1%β mercaptoethanol	50mM KCL 10mM Tris (pH 8.4) 0.45% Tween 20 0.2% gelatin 0.45% Triton X 60 µg/ml proteinase K
50X TAE : 40mM Tris –acetate 1mM EDTA pH 8.0		
Loading dye : 50mM Tris –Cl pH 8.0 5mM EDTA, 25% glycerol 0.2% bromophenol blue 0.2% Xylene cyanol FF		
DNA molecular weight marker: 1 Kilobase (1kb) DNA ladder of MBI Fermentas was used as marker. The ladder is formed by DNA fragments of 10kb, 8kb, 6kb, 5kb, 4kb, 3.5kb, 2.5kb, 2kb, 1.5kb, 1kb, 0.75kb, 0.5kb, and 0.25kb.		

b. Isolation of genomic DNA

DNA was extracted from a single whitefly preserved in ethyl alcohol using DNeasy tissue kit (Qiagen). Protocol B of the DNeasy tissue kit was followed for DNA extraction. The detailed standardized protocol is as follows.

i. Steps involved

Step 1. A single whitefly was ground in liquid nitrogen, using a tooth pick in 1.5ml eppendorf tube into which 180 μ l of ATL buffer and 20 μ l of proteinase K were added. The sample was vortexed for 20 sec. and incubated for 30min. at 55°C in a shaking water bath until the tissue was completely macerated. Vortexing was carried out intermittently during incubation time so as to disperse the sample properly.

Step 2. 4 μ l of RNase (100mg/ml) was added to the sample and was mixed by vortexing and incubated at room temperature for 5 min. Then the sample was vortexed for 15 sec. 200 μ l of AL buffer was added and mixed thoroughly by vortexing and incubated at 70°C for 10 min. Then 200 μ l of ethyl alcohol was added, mixed thoroughly by vortexing, pipetted into DNeasy spin column placed in a 2ml collection tube and centrifuged for 1min. at > 6000g (8000 rpm). Flow through and collection tube were discarded.

Step 3. DNeasy spin column was then placed in a 2ml collection tube, 500 μ l buffer AW1 was added and centrifuged for 1min. at > 6000g (8000 rpm). Flow through and collection tube were discarded.

Step 4. DNeasy spin column was placed in a 2ml collection tube, 500 μ l buffer AW2 was added and centrifuged for 3min. at 20000g (14000 rpm) to dry the DNeasy membrane. Flow through and collection tube were discarded.

Step-5 DNeasy Mini spin column was placed in a clean 1.5ml eppendorf tube and 50 μ l of AE buffer was directly pipetted out to the DNeasy membrane. This was then incubated at room temperature for 1 min. and then centrifuged for 2 min. at > 6000g (8000 rpm) to elute.

ii. Spectrophotometric estimation: 5 μ l of DNA was diluted to 500 μ l with AE buffer. Absorption was read at 260nm and 280nm using AE as reference in a UV

spectrophotometer having 1 cm path length. Concentration of the DNA in the sample was calculated using the formula $25 \mu\text{g of DNA}/0.5\text{ml} = 1 \text{ OD at } 260 \text{ nm}$.

iii. Agarose Gel electrophoresis: 5 μl of genomic DNA or PCR product was mixed with 1 μl 6X loading dye and 14 μl of sterilized water to make 20 μl volume and were electrophoresed in 1 per cent agarose gel prepared in 1X Tris-acetate–EDTA (TAE) buffer containing ethidium bromide (0.5 $\mu\text{g}/\text{ml}$). The electrophoresis was done at 52mV using 10X TAE running buffer and 1kb DNA ladder (MBI Fermentas) was used as marker. After electrophoresis, the gel was viewed in UV trans illuminator and band patterns were recorded in gel UV Vis (Mitsubishi) documentation system.

c. PCR analysis

i. Development of PCR profiles: Operon primers A1-20, B1-20, C1-20, D1-20, E1-20, F2, F12, H9 and H16 amounting to a total of 104 primers were used (Table 3). Each primer was screened for amplification of the four populations and reproducibility of PCR profiles were checked by performing PCR for a minimum of three times per primer, totaling to 1248 reactions. Total reaction mixture volume was 50 μl which consisted of 1 μl (150ng) DNA, 5 μl Taq buffer, 7 μl 3.5mM MgCl_2 , 1 μl dNTP 10mM, 1 μl primer, 1 μl Taq polymerase 500u, and 34 μl dd water. A 40 cycle PCR program lasting 4h and 38 min. was programmed on the Biometra Thermocycler and amplification was done using following profile: one cycle of 94°C for 5 min., one cycle at 38°C/40°C for 2 min. and 72°C for 3 min., followed by 39 cycles at 94°C for 1 min. 40°C for 1.5 min. and 72°C for 2 min. PCR products were examined in 1% agarose gel electrophoresis. Gel was observed under UV illuminator for PCR profiles. Photographs were taken using the gel documentation system and using Photoshop 7, and images were made into negative gray scale to make the bands more distinct.

ii. Scoring and Data analysis: The bands obtained through PCR were scored as plus and minus by visual screening. Each amplification product was considered as RAPD-PCR marker and scored across all samples. Data was entered using a maximum in which all observed bands or characters were listed. The RAPD-PCR pattern of each isolate was evaluated assigning 'character state' to all bands that could be observed in gel with certain primers. The character state '1' was given if this band could be reproducibly detected in all RAPD-PCR analyses with this isolate/ primer combination. The character state '0' was assigned if it was not possible to determine it with certainty. The data matrix thus generated was evaluated in pair wise comparisons using Jaccard's similarity coefficient calculated as per the formula $\text{Similarity Coefficient} = a/n$, where, a = number of matching bands for each pair of comparisons and n = total number of bands in the two samples observed. These similarity coefficients were subjected to Unweighted Pair Group Method on Arithmetic Averages (UPGMA) cluster analysis to group the isolates based on their overall similarities. NTSYS-PC version 1.6 software was used for this analysis.

3.3. Virus Transmission studies

a. Acquisition of virus by the vector

Virus transmission studies were focused exclusively on *Mungbean Yellow Mosaic India Virus* (MYMIV). Healthy whiteflies were raised in brinjal, cotton, okra and soybean for a period of six months and acquisition access period of 24h was given on infected mungbean seedlings (Fig. 31-1). One single whitefly placed in a 1.5ml eppendorf tube was allowed to feed on MYMIV infected seedlings. Likewise four whiteflies in four eppendorf tubes were maintained as replicates for the four populations. These infected whiteflies from each replication were then individually allowed to feed on healthy mungbean (cultivar TS 16) and soybean seedlings for 24h (inoculation access period).

These were then maintained in insect proof acrylic cages. Seedlings were observed at periodic intervals for the symptoms of the disease and its intensity.

b. Detection of virus

i. PCR detection of the viral DNA in the vector: DNA was extracted from the whitefly samples, in the manner carried out for genomic DNA extraction for molecular studies. Specific PCR was carried out for the detection of MYMIV using a primer, which can amplify the open reading frame AC2. 100-150ng of DNA was subjected to specific PCR for detection of MYMIV. The primer used was AC2 forward (5'AGGGATCCAGCGGAATTCTA3'), and AC2 reverse primer (5'AAGTCGACTTACGGAAGATCG 3'); A 30 cycle PCR program lasting 3h and 30 min. was programmed on the Biometra Thermocycler. Amplification was done using the following profile: one cycle of 94°C for 2 min., followed by 29 cycles of 94°C for 1 min., 55°C for 2 min., 72°C for 3 min. and finally extension of 72°C for 10 min. PCR product was examined through agarose gel electrophoresis for which the procedure followed as same as given in molecular studies.

ii. PCR detection of the viral DNA in the plant: Studies were simultaneously done to find out whether the whitefly has transmitted the virus to mungbean and soybean seedlings through viral DNA extraction and specific PCR for MYMIV detection. Such studies were repeated for all the four populations collected from brinjal, cotton, okra and soybean. Leaf samples from seedlings subjected to inoculation formed the sample of the study. Modified CTAB method was followed for the viral DNA extraction. DNA was extracted from young unfurling leaves of inoculated seedlings, of which details are given below:

100 mg leaf sample was ground with liquid nitrogen and the powder was transferred into an eppendorf tube containing preheated 1ml DEB buffer. This was then

incubated at 65°C for 1 hr in water bath and 667µl chloroform: isoamyl alcohol was added. Mixing was thoroughly done by inverting the eppendorf tube for 15-20 min. and was centrifuged at 10000 rpm at 4°C for 10 min. Supernatant was taken and two thirds volume of cold isopropanol was added. Gentle mixing was carried out in order to precipitate the nucleic acid. Dense clump of nucleic acid was observed and it was centrifuged at 10000 rpm at 4°C for 10 min. Supernatant was discarded, pellet was washed with 200µl of 70% ethyl alcohol and centrifuged at 10,000 rpm at 4°C for 10min. Supernatant was discarded and the pellet was dissolved in sterile double distilled water or TE buffer. Specific PCR was performed for detection of the virus in the host with the ORF AC2 primers as given under PCR studies done on the vector.

Results

4.1. Morphometric studies

4.1.2. One-way single factor ANOVA (Analysis of variance)

4.1.2.1. Puparia

4.1.2.1.1. Simple measurements

A total of 77 characters were taken up for morphometric studies on the puparia of *B. tabaci* and it was observed that many of these are neither uniform, stable, consistent nor amenable for measurement. These were confirmed by repeated trial runs undertaken with five puparia each for all the populations. The details of these characters are given in Table 1 and Fig. 1

These results indicate that, in spite of these characters being utilized by various whitefly taxonomists for defining *B. tabaci*, these are not of morphometric significance and any study focused towards the host related morphological or phenotypic variations shall take cognizance of this fact and shall proceed only after further confirming these details on the various populations. These results also reveal that it will be advisable to refrain from using these characters in the definition of *B. tabaci*; if at all it is indispensable to use them, it must be done with caution.

Out of the 39 characters subjected to one way single factor ANOVA for their statistical significance in differentiating the populations it was observed that 37 characters showed significant variations between the four populations of *B. tabaci* in terms of F values, at the probability levels above 0.01 and 0.05. Only these 37 characters had been isolated for detailed explanations, interpretations and further discussion, and these had been designated as Group of 37 characters (G37) (Table 4,5; Fig. 2-6). The remaining

two characters showed non-significant F values and the details of these characters are given in Table 4.

The two non-significant characters are breadth of abdominal segment 7 (Table 24), and that of lingula (Table 38). Thus it can be seen that both these are on the dimension of breadth alone and mainly belong to the abdominal segment 7 and lingula. The probability levels at which these characters can turn significant vary between 0.07 and 0.32, indicating their absolute invalidity in statistically defining the populations as morphologically distinct units. These results reveal that though these characters are important in the taxonomic and morphological aspects of *B. tabaci*, and other related whiteflies, when turned into measurements and analyzed for morphometrics have no significance in distinguishing the populations occurring on the four crops. Of these two, the character of breadth of lingula at base can be considered marginally distinct, as it is significant at the probability level of 0.07 and must be considered with caution as far as future studies on morphometrics of populations is concerned.

As far as the G37 characters are concerned, the statistical significance indicates that these populations are quite different from each other, and the deviation between the populations with respect to these characters is drastic, thereby signalling that the populations from brinjal, cotton, okra and soybean are transforming into morphologically and taxonomically distinct entities. For the purpose of convenience in discussing the results, these G37 characters had been categorized under three groups namely, Group of 14 (G14), Group of 21 (G21) and Group of 2 (G2) characters based on the probability levels at which these are statistically significant (Table 4).

i) Group of 14 (G14)

These are characters that show significant variations, between the populations, at the probability levels of 2.14×10^{-11} and above (Table 4,5). In statistical terms these have extraordinarily high level of significance as the F values of their variations fall between 20.58 and 481.95, which are much higher than their critical F values. Hence, these characters can be considered as very highly significant and important for the distinction of the populations morphologically. This group can be further subdivided as follows taking into account their statistical significance.

- a) The characters which show statistical significance at probability levels of 9.3×10^{-22} and above; there are six characters which come under this subgroup. These characters namely, breadth of submargin; breadth of caudal setae; breadth of caudal furrow at the middle, at apex, and at base; and breadth of abdominal segment 8 stand out due to their statistical significance at extremely high levels of probability namely, 3.57×10^{-85} (F value 481.95), 9.26×10^{-67} (F value 335.06), 2.04×10^{-32} (F value 81.34), 7.5×10^{-28} (F value 65.01), 3.15×10^{-26} (F value 59.98) and 9.3×10^{-22} (F value 46.57) respectively (Tables 10,39,29,28,30 and 26). These probability levels, according to the statistical parlance are very highly significant, resulting in the calculated F value soaring much higher than the critical F value.
- b) Breadth of submargin and that of caudal setae deserves a special mention here as these show exceedingly high level of significance at a probability level as high as 3.57×10^{-85} and 9.26×10^{-67} , respectively. If one sees the actual mean values of breadth of submargin, it could be seen that these are 9.67, 6.58, 7.02 and 4.53

units for the populations on brinjal, cotton, okra and soybean, respectively (Table 10). For these populations, the actual mean values of the breadth of caudal seta are 1.14, 2.00, 1.00 and 2.00 units (Table 39), respectively. These results and observations reveal that breadth of submargin and caudal setae could be the two characters that will be of great use in distinguishing the four populations as distinct taxonomic entities. It could also be observed that though the two characters are good in discriminating the populations, in terms of utilization of mean values for discrimination, it is only the breadth of submargin which can provide distinction of all the populations equally and clearly, indicating the superior and practical utility value of this character.

- c) Among the other four characters, are the caudal furrow's breadth at various positions (Tables 28,29,30) and that of abdominal segment 8 (Table 26); these establish the importance of caudal furrow as one of the important and distinctive taxonomic character. As far as the caudal furrow is concerned the breadth at middle is more important as it is showing variations at a high level of significance with an F value of 81.34 significant at a probability level of 2.04×10^{-32} (Table 29). The breadth at apex and at base are relatively less superior in discriminating the populations; their significance being at probability levels of 7.5×10^{-28} and 3.15×10^{-26} , respectively (Table 28,30). The breadth of abdominal segment 8 is the other character to fall in line with the above, with its significance being at the probability level of 9.3×10^{-22} (Table 26). The mean values of the breadth of caudal furrow at middle range between 3.04 and 4.61 units for the four populations from brinjal, cotton, okra and soybean, with latter being the maximum and the okra the least. The differences in these mean values are quite obvious and

can be readily deployed for the differentiation of the populations. Likewise the breadth of caudal furrow at apex has its mean values ranging between 3.06 for okra to 4.53 units for the soybean populations, while its breadth at base varies between 3.02 for brinjal and 7.58 for the soybean populations. These indicate that soybean had profound effect on the breadth of caudal furrow effecting significant taxonomic variations.

- d) There are eight characters which fall under G14 ranking next to the above six characters in terms of their F values significant at probability levels ranging between 5.62×10^{-16} and 2.14×10^{-11} (Table 32,43,16,35,27,8,31,12). Among these the breadth of operculum at apex stands out due to its high F value namely 31.45 significant at probability level of 5.62×10^{-16} . Similarly, the characters namely, breadth of vasiform orifice near base, and that of abdominal segment 3 have their F values significant at the probability levels of 1.24×10^{-14} and 6.36×10^{-14} (Table 43,16); length of lingula is the other character, which falls in the similar level of significance with its F value being 24.96 significant at the probability level of 3.24×10^{-13} (Table 35).
- e) Similarly length of caudal furrow, breadth at middle of puparia, length of operculum and breadth of abdominal segment 1 stand out due to their statistical significance at extremely high levels of probability namely, 1.64×10^{-12} , 2.84×10^{-12} , 4.79×10^{-12} and 2.14×10^{-11} , respectively (Tables 27,8,31,12). These results also indicate that all these characters are almost on par with each other in discriminating the populations as distinct morphological entities., as their F values range between 23.18 and 20.58. These also indicate that the extent of variation in these characters in the four populations is influenced through a similar degree.

ii) Group of 21 (G21)

- a) The second subgroup of G37 includes, twenty-one characters, which show statistical significance at the probability levels between 1.41×10^{-10} and 6.01×10^{-4} with their F values ranging between 19.09 and 6.06. Among these are ten characters from the abdominal segments namely, breadth of abdominal segment 2, 4, 5 (Table 14, 18, 20) and length of abdominal segments 1, 3, 5, 4, 6, 7, 8 (Table 11, 15, 19, 17, 21, 23, 25). Also, among these are characters located on the vasiform orifice (3), lingula (2), operculum (2), besides breadth at apex and length of puparia as a whole. Though these characters are of lesser significance when compared to the G14 characters explained above, the significance levels are indeed extremely high in statistical parlance and all these characters have great value in distinguishing the populations.
- b) The character which shows highest level of statistical significance in this subgroup are breadth of vasiform orifice at apex (Table 41); of puparia at base (Table 9); of lingula at middle (Table 37); breadth of operculum at base (Table 34), and that of breadth of abdominal segment 2 (Table 14) with the levels of probability at which F being significant ranging between 1.41×10^{-10} and 7.29×10^{-10} . If we consider these 16 characters as a whole, it is evident that the maximum numbers of these characters are on the abdomen, which indicates that to distinguish the populations, importance must be given to the study of characters on the abdomen.
- c) The characters under this group are all mega characters that have superior morphometrical discriminating potential to distinguish the four populations. These results also reveal that the dimension of breadth in *B. tabaci* is influenced to a much lesser degree by the four host plants namely brinjal, cotton, okra and

soybean. This also emphasizes the fact that morphometrics in terms of the dimension of breadth is more important than length in case of many characters that are taxonomically important in puparia.

iii) Group of 2 (G2)

- a) Those two characters, which show the significant variation, between the four populations, at the probability levels ranging from 0.05 to 0.02, fall under this category (Table 22,40). These have their variations with their F values range between 2.72 and 3.38, and include breadth of abdominal segment 6 and length of vasiform orifice. The mean values of breadth of abdominal segment 6 is found to vary a 12.00, 11.87,11.27 and 10.65 units (Table 22), while that of length of vasiform orifice varied as 27.51,29.27,27.97, and 29.90 units, respectively for brinjal, cotton, okra and soybean.

4.1.2.1.2. Ratios of measurements

The one way single factor ANOVA carried out with regard to the ratios between the selected characters indicate that except for the dimension of length vs. breadth of puparia, all other ratios between the different body parts are significantly different for the four populations (Table 45). The variations in the ratios between the length vs. breadth of abdominal segment 8 and those of caudal furrow showed the highest significance with F values of 23.75 and 22.91, respectively. With the level of probability at which these are significant being at the levels ranging between 3.7×10^{-13} and 9.5×10^{-13} , these are slated to be few of the morphometric characters for the distinction of the four populations. The ratios between the length and breadth of vasiform orifice, abdominal segment 1 and 7 are the next in line with probability levels at which these are significant hovering between 6.69×10^{-7} and 3.3×10^{-6} . The ratios between length and breadth of abdominal segments

2,4,3,5 and 6 ranked next with their F values ranging between 3.36 and 7.40 with their level of significance being at probability levels between 1×10^{-3} and 1×10^{-5} . These results also indicate that the characters in the abdomen play a significant role in morphometrics of puparia of *B. tabaci* and in differentiating the four populations.

4.1.2.1. Adults

4.1.2.1.1. Simple measurements

A total of 24 characters were taken up for morphometric studies on the adults of *B. tabaci* and it (Table 2) was observed that many of these are neither uniform, stable, consistent nor amenable for measurement. These were confirmed by repeated trial runs undertaken with five adults each for all the populations. These observations indicate that, in spite of these characters being utilized by various whitefly taxonomists for defining *B. tabaci*, these are not of morphometric significance and any study focused towards the host related morphological or phenotypic variations shall take cognizance of this fact and shall proceed only after further confirming these details on the various populations. These results also reveal that it will be advisable to refrain from using these characters in the definition of adults of *B. tabaci*; if at all it is indispensable to use them it must be used with caution.

Out of the 10 characters subjected to one way single factor ANOVA for their statistical significance in differentiating the populations it was observed that 8 characters showed significant variations between the four populations of *B. tabaci* in terms of F values, at the probability levels above 0.01 and 0.05 (table 46-57; Fig. 7). Only these 8 characters had been isolated for detailed explanations, interpretations and further discussion, and these had been designated as Group of 8 characters (G8) (Table 46,47).

The remaining two characters showed non-significant F values and the details of these characters are given in Table 46.

The two non significant characters are breadth of compound eye (Table 51) and that of proboscis (Table 53). Thus it can be seen that both these are on the dimension of breadth alone and the probability levels at which these characters can turn significant vary between 0.07 and 0.47, indicating their absolute invalidity in defining the populations as morphologically distinct units. These results reveal that though these characters can turn out to be important in the event of utilizing the taxonomic and morphological aspects of adults of *B. tabaci*, and other related whiteflies, when turned into measurements and analyzed for morphometrics have no significance in distinguishing the populations occurring on the four crops.

As far as the G8 characters are concerned, the statistical significance indicates that these populations are quite different from each other in these, and the deviation between the populations is drastic, thereby signaling that these populations are transforming into morphologically and taxonomically distinct entities (Table 48-50,52,54-57). For the purpose of convenience in discussing the results, these G8 characters had been categorized under two groups namely, Group of 7 (G7) and Group of 1 (G1) characters based on the probability levels at which these are statistically significant.

(i) Group of 7 (G7)

These are characters that show significant variations, between the populations, at the probability levels of 5.27×10^{-6} and above (Table 46). In statistical terms these have extraordinarily high level of significance and hence are extremely significant and important characters. This group can be further subdivided as follows taking into account their statistical significance.

- a) The characters which show statistical significance at the probability levels of 4.31×10^{-17} and above; there are four characters which come under this subgroup. These characters namely, length of head, breadth of thorax, length of thorax and length of abdomen stand out due to their statistical significance at extremely high levels of probability namely, 2.86×10^{-77} (F value 338.78), 2.15×10^{-31} (F value 71.87), 5.86×10^{-20} (F value 39.37) and 4.31×10^{-17} (F value 32.49), respectively (Tables 48,55,54,56). These probability levels, according to the statistical parlance are very highly significant, resulting in the calculated F value soaring much higher than the critical F value. Length of head deserves a special mention here as it shows exceedingly high level of significance at a probability level as high as 2.86×10^{-77} . If one sees the actual mean values of length of head, it could be seen that these are 37.66, 63.86, 57.68 and 39.40 for the populations on brinjal, cotton, okra and soybean, respectively (Table 48). This result and observation reveal that length of head could be a single character that will be of great use in distinguishing the four populations as distinct taxonomic entities. The ratio of this morphometric character for the four populations is significant at a probability value of 3.04×10^{-9} and F-value of 15.8, indicating the utility value of this character. Similarly, the characters namely, breadth and length of thorax and length of abdomen stand out due to their statistical significance at extremely high levels of probability namely, 2.15×10^{-31} , 5.86×10^{-20} and 4.31×10^{-17} , respectively (Table 55,54,56). Among these, two characters are from the thorax indicating that morphometrics of thorax could play very useful role in distinguishing the populations, morphometrically and taxonomically.

- b) The characters, which show statistical significance at the probability levels between 1.46×10^{-7} and 3.00×10^{-4} are the next in rank, which include length of compound eye, breadth of abdomen and head, and length of proboscis (Table 50,57,49,51). All these from the head region and indicate that in case of adults of the whiteflies, it is rather head than abdomen which shows morphometric variations significantly.

4.1.2.1.2. Ratios of measurements

Table 58 provides the list of the ratios used in the morphometrics of adults and their significance. It can be observed that the ratios between the length and breadth of proboscis provides the most significant dimension (at probability level of 1.6×10^{-120} and F value of 1108.6) which could be exploited to distinguish the four populations of *B. tabaci* occurring in brinjal, cotton, okra and soybean. The one way single factor ANOVA carried out with regard to the ratios between the selected characters indicate all other ratios between the different body parts are also significantly different for the four populations. The variations in the ratio between the length vs. breadth of abdomen showed significance at the probability level of 1.07×10^{-43} after proboscis indicating the value of abdomen as in puparia. The ratios between the length and breadth of thorax and head showed significance with F values of 16.29 and 15.80, respectively, while those of compound eye showed a F value of 6.17 significant at the probability level of 4×10^{-4} .

4.1.3. Coefficient of variation

With an objective of getting information on the validity of the morphometric characters utilized in the present study, statistical analyses were undertaken on the characters which had shown significance with ANOVA, for evaluating the extent of variation within the populations. The coefficient of variation (CV) had been selected as

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the index of variation that is within; those that have a higher CV values are much variable within and hence are not dependable in differentiating the populations. The results obtained on their variability within, with respect to the characters of morphometrics in the puparia and adults of the four populations, which had shown significance in their ANOVA are discussed below.

4.1.3.1. Puparia

The coefficient of variation for the 37 characters found significant for the variations through one-way single factor ANOVA, ranged from a minimum of 8.06 per cent for the breadth of vasiform orifice at base (Table 44) to a maximum of 42.95 per cent for the breadth of caudal furrow at base (Table 30). These indicate that all the 37 characters that showed significant variations, in the ANOVA, between the four populations are not equally fit to be used as stable characters to distinguish the populations as distinct morphological and taxonomic entities. Among these 37 characters, two characters had their coefficient of variation below 10 per cent for all the four populations at any one time; 32 characters had their CV values between 10.61 (Table 6) and 18.23 per cent (Table 22); two characters had their CV as 30.35 (Table 26) and 13.81 per cent (Table 28), while one had its CV reaching 42.95 per cent (Table 30), when all the populations are considered together for the variation within, in the characters significant in their F values.

(i) G14 characters and CV values

Of the 37 characters which showed statistical significance, out of 39 characters analyzed for single factor ANOVA, at the probability level above 0.05, when analyzed for their CV, individually for the four populations separately and all the four together, it could be seen that the breadth of submargin (Table 10) showed highly significant F value

for the separation of the four populations from the different crops as distinct morphological and taxonomical units. At the same time this character showed a CV value of 9.36 per cent for all the four populations put together. The significance of F value (481.95) of this character is at an extremely high level of probability of 3.57×10^{-85} ; these observations point to the fact that the character, breadth of submargin of puparia is a reliable, consistent and stable taxonomic character which could be exploited for the separation of the populations from brinjal, cotton, okra and soybean as distinct morphological entities. Even while considering the populations individually from brinjal, cotton, okra and soybean except for the latter for all the other three populations, the CV value was less than 10 per cent i.e., 7.49, 8.36, and 9.42 per cent respectively; only for soybean the CV was 14.57 per cent which is though on comparative terms higher, the character can be considered highly stable and viable for the discrimination of the four populations as distinct taxonomic entities.

If we consider the remaining thirteen characters of the first subgroup G14, except for the three characters namely breadth of abdominal segment 8 (Table 26), that of caudal furrow at apex (Table 28) and at base (Table 30), all other characters had their CV values between 9.36 and 13.71 indicating their considerable stability and consistency in the nature of these characters and their utility in distinguishing the four populations as distinct taxonomic entities. These kinds of low CV values, for such statistically high level of significant characters, add more value for their exploitation in the separation of the populations into morphologically and taxonomically distinct entities.

As regards the second subgroup of G21, i.e., a group of twenty one characters of which the ANOVA is significant at the probability levels between 1.41×10^{-10} and 6.01×10^{-4} , it was observed that the CV values are ranging between 10.82 (Table 41) and

11.92 (Table 14). There are thirteen characters in this group, which have their CV values around 10 to 15 per cent, indicating their consistency and reliability of these characters for the distinguishing of the four populations of *B. tabaci*. These characters include length and breadth of puparia (at apex, base), breadth of vasiform orifice, lingula and operculum; breadth of abdominal segment 2, 5; and length of abdominal segments 1,2 and 3 indicating that it will be worthy to bank upon these characters for the distinction of the populations as distinct morphological entities. There are seven characters under this subgroup namely length of abdominal segments 4 to 8, breadth of abdominal segment 4 and that of operculum at base (Table 17,18,19,21,23,25,34) for which the CV values are ranging between 15.26 and 18.11 for all the populations when considered together, which are the next best characters as far as the consistency of the characters are concerned. These again indicate the importance of the abdomen as the most important taxonomic aspect of *B. tabaci* exhibiting variability that could be easily exploited for morphometrics.

(ii) G2 characters and CV values

For the two (G6) taxonomic characters which showed statistical significance at probability levels between 0.05 and 0.02, the coefficient of variation was found to vary between 10.93 and 18.23 per cent. Amongst these two characters, in case of length of vasiform orifice, the CV values were hovering between 10 and 11 per cent. These results had indicated that the variations within are the least and confirmed its usefulness in distinguishing the populations as distinct morphological and taxonomic entities.

4.1.3.2. Adults

The results on the variability of adults with respect to the eight characters of morphometrics in the four populations from brinjal, cotton, okra and soybean, which had shown significance in their ANOVA, are discussed below.

The coefficient of variation for the eight characters varied from a minimum of 9.26 per cent for the length of proboscis (Table 52) to a maximum of 21.11 per cent for the breadth of abdomen (Table 57). These indicate that all the eight characters, which showed significant variations, in the ANOVA, between the four populations, are not equally fit enough to be used on par as stable characters to distinguish the populations as distinct morphological and taxonomical entities. Among these eight characters, length of proboscis had its coefficient of variation hovering around 10 per cent for all the four populations (Table 52); the CV values being 8.11, 8.76, 11.50 and 8.56 per cent for the populations from brinjal, cotton, okra and soybean, respectively and 9.26 per cent for all the populations altogether. This had brought out the fact that it is a much reliable character for the distinguishing the populations at the adult stage, in spite of its statistical significance in terms of single factor ANOVA being the least of all. The length of compound eyes is the next best character (Table 50) with its CV value being only 9.94 per cent. The length of head (Table 48) ranked third among the eight characters in terms of consistency within the populations and showed CV values of 10.53, 11.16, 8.12 and 9.12 per cent for the brinjal, cotton, okra and soybean populations, respectively. The length of abdomen (Table 56) and breadth of thorax (Table 55) are the characters with their CV values between 13.92 (Table 56) and 13.81 per cent (Table 55). These characters had their CV values as 14.69, 13.13, 14.29, 13.01 and 10.70, 15.46, 15.66 and 8.53 per cent for the populations from brinjal, cotton, okra and soybean, respectively, which indicate that these characters have great scope in defining the four populations morphometrically and taxonomically.

There is one character, which exhibited variations within the individual populations to the extent of reaching the CV values of more than 20 per cent; it is the breadth of abdomen (Table 57), wherein the CV values for all the populations considered

together reached 21.11 per cent. All these results indicate that these characters of the adults of *B. tabaci* are considerably and comparatively much variable and are to be used with caution in distinctly defining the four populations as taxonomic entities, though these are exhibiting significant variations in terms of F values over single factor ANOVA tests.

4.1.4. Analysis of least square differences of means

4.1.4.1. Puparia

There are six characters namely breadth of puparia at apex, of submargin that of caudal furrow at apex, length of operculum and breadth of vasiform orifice near base which have their means/least square mean values distinct from each other. These characters can be utilized to separate the four populations obtained from the crops namely brinjal, cotton, okra and soybean for distinguishing purposes. It will be worthwhile to note that four of these characters fall in the category of G14 and two in the category of G21, as far as the significance of its values are concerned, when analysed for Single Factor ANOVA. It will also be worthwhile to observe that except for the breadth of caudal furrow at apex, all other characters have their co-efficient of variation ranging between 9.36 and 13.71 when all the populations were considered together. All these indicate that these characters are unique with respect to their statistical significance in these variations persistent to a population of a specific host and are also consistent and persistent within them. From these it can be concluded that these characters can be safely identified for the distinction of the populations. The least square differences in the means of various characters and their comparisons with regards to each host in terms of their distinction are given in Table 59. When any character is to be utilized for a population from a particular host it will be appropriate to use these differences.

4.1.4.2. Adults

There is no morphometric character in the case of adults which gets isolated in terms of least square differences of means over the four different populations from brinjal, cotton, okra and soybean, making their distinction amply evident (Table 60). For e.g., with regard to length of head and breadth of thorax, means are at par in the populations from brinjal and soybean, while those from cotton and okra are distinct from each other; length of compound eyes and breadth of abdomen in brinjal and cotton are at par with each other while those from okra and soybean are at par with each other. As far as the length of thorax is concerned brinjal with okra and cotton with soybean are at par with each other; in the case of the length of abdomen the populations from brinjal and okra are at par but significantly distinct from those of soybean. These observations indicate that the host related variations in definite morphological dimensions in adults are not to the same degree as seen in the case of puparia. It will be worthwhile to bank upon the morphological dimensions of puparia rather than adults for definite interpretations on the host related phenotypic variations in *B. tabaci*.

4.1.5. Correlation coefficient analyses

4.1.5.1. Puparia

Simple correlation studies were undertaken on the 39 characters of the puparia analyzed for the one way single factor ANOVA, to ascertain the relationship among these characters. This was done for the four populations from brinjal, cotton, okra and soybean separately and by taking all the populations as one group so that interpretations based on their significance could be drawn for the species *B. tabaci* as a whole (Table 65a-d). The salient findings of these analyses are as follows:

- a) There are 562 negative correlations in the relationships between the characters in the four crops, of which the majority of 441 are confined to the populations from cotton and soybean, indicating that the morphometric behaviour of these populations is quite different from the crops namely brinjal and okra (Table 70a). It was also observed that many of these are significant at high probability levels (> 0.001). Of these, particularly the characters in the abdomen including those of the different abdominal segments and those of the caudal furrow, operculum, lingula and vasiform orifice had the majority of their relationships with each other negative, indicating that these are more significant in affecting the relationships between the characters and hence are very important in the phylogenetic analyses. Thus, the populations from cotton and soybean gets isolated from those of brinjal and okra and the general trend that we get by pooling all the populations together as one compact unit. These results also point to the fact that these morphometric relationships isolate populations from cotton and soybean as distinct taxonomic entities and hence the 37 characters significant through one way single factor ANOVA could be conveniently used to distinguish these populations as morphologically and taxonomically distinct units.
- b) It was observed that there were 116 negative relationships among the total of 741 relationships between the different morphometrics when we consider the populations from all the four crops together. It can also be concluded that the populations from cotton and soybean rather than brinjal and okra contribute towards the negative correlations, which we get in the pooled populations. The drastic variations in the extent of relationships between the different characters of morphometric and taxonomic significance in the pooled populations point to the fact that populations are heterologous entities and it is impossible to consider the

various populations of *B. tabaci* occurring over the four crops as monophyletic units.

- c) The populations of *B. tabaci* from soybean were observed to have the maximum number of their characters negatively correlated with each other (226 out of 741 amounting to more than 30 per cent) in comparison to other populations, indicating that this population is entirely different in terms of ecological units with variations due to the host plant relationships (Table 64 a-d). The statistical significance of these relationships when analyzed indicates that only 25 per cent are significant at probability levels of 0.05 and above. These relationships were found to encompass majority of characters, which are also found to be extremely significant characters in the one way single factor ANOVA.
- d) The populations from cotton behave similar to those on soybean with 215 (29 per cent) of their 741 relationships between the different taxonomic characters negatively correlated with each other (Table 62 a-d). The statistical significance of these relationships when analyzed indicates that more than one third of these relationships are significant at probability levels of 0.05 and above. As in the case of soybean these relationships dominate through the significant characters in the abdomen including those of caudal furrow, operculum, lingula and vasiform orifice, which were found to be the most important characters in differentiating the populations as distinct morphological and taxonomic units. This also brings out the fact that in addition to soybean it is cotton, which is able to bring out the host related phenotypic variations in *B. tabaci* in a manner, where large number of relationships are negatively correlated with each other.

- e) In case of population from brinjal 93 per cent (688 of the total 741) of the relationships between the morphometric measurements were positively related indicating that these populations are much different from those of soybean and cotton as regards their host plant relationships are concerned (Table 61 a-d). The statistical significance of these relationships when analyzed indicate that more than 90 per cent are significant at probability levels of 0.05 and above. The host relationship influence and the host related phenotypic variations in brinjal are more positively related with the actual size, and if one character decreases or increases in morphometrics, many other characters also decrease or increase as the case may be.
- f) In case of populations obtained from okra it could be seen that these are similar to those of brinjal as regards their host plant relationships are concerned (Table 63 a-d). It was seen that 673 of the 741 relationships have positive relationships. The statistical significance of these relationships when analyzed indicate that more than 60 per cent are significant at probability levels of 0.05 and above. Majority of these are positive relationships and encompassed the morphometrics of abdomen, caudal furrow, operculum, lingula and vasiform orifice.

4.1.5.2. Adults

- a) In case of adults of *B. tabaci*, the populations obtained from brinjal (Table 66) and cotton (Table 67) had more number of their relationships (33 to 40 per cent) negatively correlated with each other. In contrast, the populations from okra (Table 68) and soybean (Table 69) had majority (88 to 95 per cent) of the relationships between morphometrics positively correlated with each other

indicating that the host correlated phenotypic variations in the adults are entirely on a different note when compared to the puparia.

- b) As far as the significance of the host influenced relationships in the morphometrics of adults are concerned it could be observed that only 18 to 20 per cent of the relationships are significant in case of brinjal, cotton and soybean, and 40 per cent in case of okra. This indicates that the adults are comparatively poorly influenced by the host plant influences when compared to puparia. In case of the pooled populations from all the four crops however more than 55 per cent of the relationships were significant at probability levels of 0.05 and above, indicating that as a whole the populations of *B. tabaci* are morphometrically influenced significantly in their morphometrics by the host related phenotypic variations (Table 70).

4.1.6. MANOVA

4.1.6.1. Puparia

To know whether all the observations on the morphometrics when considered together differentiate the four populations from brinjal, cotton, okra and soybean or not, multivariate ANOVA was carried out. Various test statistics used in MANOVA along with the significance level are indicated in the Table 74. Multivariate ANOVA performed on the five principal components (PC) combined using the statistics namely Wilk's Lambda, Pillai's Trace, Hotelling-Lawley Trace and Roy's Greatest root revealed that the components of variations are significant at very high levels where probability levels far exceed 0.0001. These analyses reveal that out of the univariate ANOVA performed on the 35 PCs individually, only five PCs (Prin1 to Prin5) showed significant effect (Prin.1: $F=24.00$; $P= 0.001$; Prin.2: $F=121.00$; $P= 0.001$; Prin.3: $F=100.71$; $P= 0.001$; Prin.4:

$F=2.07$; $P=0.001$; Prin.5: $F=13.95$; $P=0.001$) (Table 73 a-e). Thus, these five PCs were able to show the significant variations among the four populations obtained from brinjal, cotton, okra and soybean. These results also clearly indicate that the populations coming from these different crops show variations in the taxonomic characters considered in puparia for identification of *B. tabaci*.

4.1.6.2. Adults

Multivariate ANOVA was performed on the three PCs combined using the statistics namely Wilk's Lambda, Pillai's Trace, Hotelling-Lawley Trace and Roy's Greatest root on the observations obtained from adults as in the case of puparia (Table 79). This revealed that all the characters show highly significant variations at the probability levels higher than 0.0001. These results revealed that out of the univariate ANOVA performed on the 10 PCs individually, only Prin 1 to Prin 3 (Table 78 a-c) showed significant effect (Prin.1: $F=84.35$; $P=0.001$; Prin.2: $F=43.25$; $P=0.001$; Prin.3: $F=11.86$; $P=0.001$). Thus, these 3 PCs were able to show the significant variations among the four populations in case of adults and these could convincingly concluded that the populations obtained from brinjal, cotton, okra and soybean are morphometrically different as in the case of puparia.

4.1.7. Principal Component Analysis

4.1.7.1. Puparia

Variables with more than 15 per cent cases missing were removed from the Principal Component (PCA) and Discriminant Function Analysis (DFA). Similarly, cases missing in more than 10 variables were removed from the analysis. The Principal Component Analysis, a multivariate statistical procedure was performed to reduce the number of variables by projecting the original measured variables into a new set of

variables that has some inherent statistical properties. In simple terms, the principal components, which are nothing but linear combinations of original variables that have special properties in terms of variances, were obtained. For example, the first principal component is the normalized linear combination (the sum of squares of the coefficients being one) with maximum variance. Since the numbers of measurements are very high, using the principal component analysis, it is possible to select first few principal components, which have large variations and could explain the differences in the populations. The Principal components extracted from the puparia measurements are listed in Table 71. The first principal component could explain more than 40 per cent of the variation. The total number of PC that could be obtained from the analysis is same as the number of variables in the study. To decide the number of principal components, two procedures are followed, namely Scree Plot technique and number of principal components whose eigen values are more than 1. In Scree Plot technique, the eigen values are plotted. The values will be decreasing at faster rate in the beginning and afterwards, the line will be more or less straight line. The number of principal components is decided from where the line is stabilized. In the present case, it is at 5. The first 5 principal components could explain more than 73 per cent of variation. Thus, 5 principal components were chosen for further study and listed in Table 72 as Prin1, Prin2, Prin3, Prin4 and Prin5. From the 37 measurements selected in the puparia, using principal components, it was possible to reduce it to five variables. The first principal components, with the exception of breadth of submargin and breadth of caudal furrow at apex, all the variables are having positive signs and able to explain 40 per cent of variation. The loadings were low to moderate, indicating some influence on the variation. The first principal component can also be termed as the average of the variables considered. The second principal component contrasts the effect of length of puparia, breadth of

abdominal segment 1, and that of segment 8, that of caudal furrow at apex, at middle, at base, length of operculum, breadth of operculum at apex, at base, length of lingula, breadth of lingula at apex, at middle, that of vasiform orifice near base, that of caudal seta, that of vasiform orifice at apex, near apex, and that abdominal segment 4.

The Fig. 8 depicts the first and third principal components. The population from soybean is distinctly seen mostly in first and fourth quadrant and they are further apart from the other three populations. This also shows that the first principal component scores for population from soybean are all positive. The population from brinjal is split both in second and third quadrant whereas population from okra is seen mostly on third quadrant. The population from cotton is sandwiched between all the other populations. The Fig. 9 shows the data on first and third principal component axis, which reveal that all the four populations are well spread here. Likewise the different combinations of principal components are depicted in Fig. 10-17.

4.1.7.2. Adults

The principal components extracted from the adults' measurements are listed in Table 76. The first principal component could explain more than 38 per cent of the variation. The total number of PC that could be obtained from the analysis is same as the number of variables in the study. To decide the number of principal components, two procedures are followed, namely Scree Plot technique and number of principal components whose eigen values are more than 1. In Scree Plot technique, the eigen values are plotted. The values will be decreasing at faster rate in the beginning and afterwards, the line will be more or less straight line. The number of principal components is decided from where the line is stabilized. In the present case, it is at 3.

The first three principal components could explain more than 68 per cent of variation. Thus, 3 principal components were chosen for further study and listed in Table

77 as Prin1, Prin2, and Prin3. From the ten measurements considered in the adults, using principal components, it was possible to narrow down to three variables. In the first principal component, with the exception of breadth of head, all the variables are having positive signs and are able to explain 38 per cent of variation. The loadings were low to moderate, indicating some influence on the variation. The first principal component can also be termed as the average of the variables considered. The second principal component contrasts the effect of length of head, length of thorax and breadth of thorax from the rest of the variables. The third principal component is found to be giving negative values in case of breadth of eyes, breadth of proboscis, length of abdomen and breadth of abdomen. Fig. 18 depicts the first and second principal components, from which it can be observed that populations from brinjal, cotton and soybean are distinctly isolated and okra is found to be distinct from brinjal and soybean alone. When plotted against principal component 1 and 3, population from soybean is found to be distinct from cotton and the same was observed when plotted against Prin 1 and Prin 4 and also when plotted against Prin 1 and Prin 5. In case of figures produced when plotted against Prin 2 to Prin3, Prin 2 vs Prin 4 and Prin 2 vs Prin 5, all four populations were found to be overlapping (Fig. 19-27).

4.1.8. Discriminant Function Analysis

4.1.8.1. Puparia

The Table 75a gives the linear discriminant function (DFA) for each crop. Using the discriminant function, each observation from different crops has been classified. The table gives the number of cases from each crop and the per cent classified into different crop has been listed. It can be seen that 45 cases from brinjal have been classified into same crop and hence all the observations have been classified correctly. Similarly, all 36

cases from cotton, all 49 cases from okra and all 31 cases from soybean have also been classified correctly. Thus, the error rates using the linear discriminant function were nil as shown in the table.

However, all the cases were used to develop the discriminant function and hence the classification based on the same data usually result in lower error rates. Hence, Jackknifed discriminant function was used to give better error estimates. This is also known as cross-validation. The summary table 75b gives the classification results based on cross-validation. Here, one observation from cotton has been classified into as coming from soybean and all other cases were classified correctly even using the cross-validation. Thus, the error rates estimated for cotton was 0.0278 while the overall error-rate was 0.0069. This shows that the discriminant function analysis has been able to differentiate the populations using the characters selected in the analysis. The discriminant function analysis also show that there exists definite distinction between the populations coming from the four different crops and that the distinction can easily be explained by the taxonomic characters selected in the study.

Thus, based on all the statistical analysis, it can be concluded that there exists definite distinction between the populations coming from the four crops. The dendrogram of relationships between the four populations is depicted in Fig. 28, which shows that the brinjal and soybean populations are closer, and branch out from those of cotton and okra.

4.1.8.2. Adults

The Table 80a gives the linear discriminant function (DFA) for each crop. Using the discriminant function, each observation from different crop has been classified. The table gives the number of cases from each crop and the percent classified into different crops. The number of observations is found to be 50. It can be seen that 35 cases from brinjal have been classified into same crop while 15 has been classified under soybean.

Similarly, all 37 cases from cotton were noted under cotton and 13 under okra. 40 cases of okra have also been classified correctly while 10 cases were found under cotton. In respect of soybean, 45 cases were found under soybean while 5 were located under brinjal. Thus, the error rates using the linear discriminant function were found to be higher than that observed in case of the analysis carried out in case of puparia obtained from the four different crops.

However, all the cases were used to develop the discriminant function. Hence, Jackknifed discriminant function was used to give better error estimates. This is also known as cross-validation. The summary table 80b gives the classification results based on cross-validation. Here, one observation from cotton has been classified into as coming from soybean and all other cases were classified correctly even using the cross-validation. Thus, the error rates were estimated for brinjal was 0.30, cotton 0.26, okra 0.20 and 0.10 soybean and an overall error-rate was 0.21. This shows that the discriminant function analysis has been able to differentiate the populations using the characters selected in the analysis. The discriminant function analysis also shows that there exists definite distinction between the populations coming from the four crops.

4.2. Molecular Studies

The objective of the molecular studies was to develop a nucleic acid based molecular marker for identification and differentiation of populations of *B. tabaci*. The study involved populations isolated from brinjal, cotton, okra, and soybean on which morphometric studies have been done. Details of sampling and maintenance of the populations are as given in Material and Methods. Standardization of protocol for isolation of genomic DNA, optimization of various parameters for RAPD-PCR and analysis profiles of DNA was undertaken.

4.2.1. Standardization of protocol for isolation of Genomic DNA

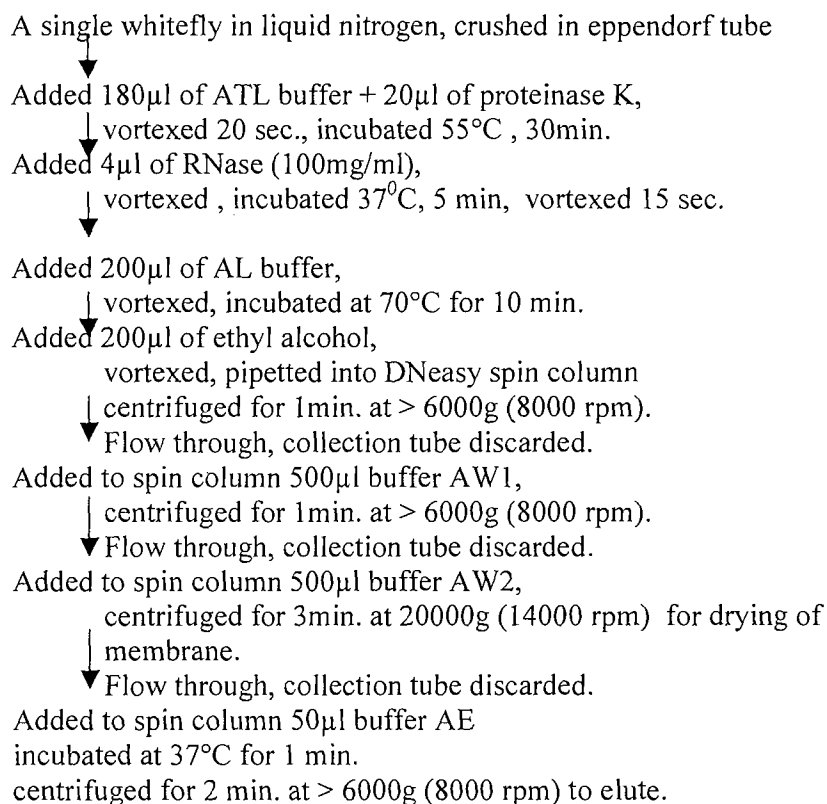
Populations from cotton were used in all the standardization experiments. Initially a single whitefly was frozen in liquid nitrogen and ground into powder in an eppendorf tube with a toothpick. Whenever more than one whitefly was used, group of two, five, eight and ten whiteflies were frozen in liquid nitrogen and the powder suspended in extraction buffers. Protocol to isolate RAPD-PCR compatible and good quality DNA was standardized after evaluating different buffers and procedures, as follows:

- a) **2% Cetyl Trimethyl Ammonium Bromide (CTAB) Method:** This method is modified from Dellaporta *et al* (1983). A single whitefly ground into powder in liquid nitrogen was suspended in an equal amount (w/v) of CTAB buffer and incubated at 65°C for 1h. The suspension was centrifuged in a Sorvall RC-5C centrifuge by using SS-34 rotor at 15,000 rpm for 20 min. at 20°C. The supernatant was transferred into sterile centrifuge tube and mixed gently with equal volume of chloroform: isoamyl alcohol (24:1). The mixture was centrifuged at 15,000 rpm for 20 min. at 20°C. The supernatant was transferred into sterile tubes and again mixed with chloroform: isoamyl alcohol (24:1) and the process was repeated until the aqueous phase was clear. To the final aqueous phase, 0.1 volume of sodium acetate ($\text{CH}_3\text{COONa} \cdot n\text{H}_2\text{O}$) 3M, pH 4.8 and 0.8 volume of isopropanol were added and kept overnight at -20°C for precipitation. The precipitate was then centrifuged at 15,000 rpm for 30 min., the pellet washed with 70% ethyl alcohol, air dried and dissolved in 80µl of resuspension buffer (1X TE, pH 8.0). 5µl of the isolated DNA was electrophoresed to check the DNA. No genomic DNA band was visible by using this method. 1µl of the isolated DNA taken up for PCR reaction provided no amplification.

- b) **Modified 2% CTAB Method:** The extraction buffer was preheated at 65°C for 15 min. in shaking water bath. A single insect was ground with liquid nitrogen and the powder was transferred into an eppendorf tube containing preheated 1ml of DEB (modified 2%CTAB). This was incubated at 65°C for 1 h in water bath and 667µl chloroform: isoamyl alcohol was added. Mixing was thoroughly done by inverting the eppendorf tube for 15-20 min. and then centrifuged at 10,000 rpm at 4°C for 10 min. Supernatant was added with two thirds volume of cold isopropanol and gentle mixing was carried out to precipitate the nucleic acid. Dense clump of nucleic acid was observed, which was centrifuged at 10,000 rpm at 4°C for 10 min. Supernatant was discarded, pellet washed with 200µl of 70% ethyl alcohol and centrifuged at 10,000 rpm at 4°C for 10min. Supernatant was discarded and the pellet dissolved in sterile double distilled water or TE buffer. Visualization of genomic DNA was not possible when 5µl of the isolated DNA was subjected to gel electrophoresis. 1µl of the isolated DNA taken up for PCR reaction provided no amplification.
- c) **Lysis buffer method:** Individual whiteflies were homogenized in 10µl of lysis buffer (deBarro and Driver 1997), using 1.5ml microcentrifuge tube and a 500µl pipette tip, which had been melted and then moulded to fit inside of the microcentrifuge tube. After homogenization a further 15µl of lysis buffer was added. The homogenate was then incubated at 65°C for 30min., incubated and then boiled for 10 min. to inactivate proteinase K. Sterile double distilled water was added to yield a final homogenate volume of 50 µl. 5µl of the isolated DNA was checked through electrophoresis, which did not show genomic DNA band. PCR reaction too provided no amplification.

d) **DNeasy tissue kit (Qiagen) ATL buffer:**

Steps involved (flow chart)



5µl of isolated DNA was subjected to gel electrophoresis, which revealed a clear genomic band. 1µl of DNA subjected to PCR gave amplicons with many primers.

b. Other protocol aspects:

- a) **Lysis time:** The protocol of DNeasy tissue kit has a lysis step in which after addition of extraction buffer, the suspension is kept at 55°C to allow lysis. Attempts were made to find out whether increase or decrease of lysis time would improve the DNA yield. After adding extraction buffer, lysis was allowed for 30 min. 45 min. 1h, 1.5 h, 2h and 3h after which DNA was purified through the column. Gel electrophoresis revealed that 30 min. lysis time gave good results.
- b) **Number of Insect(s):** DNA was extracted from single or a group of 2, 5, 8, 10 whiteflies in order to ascertain the quantity of insects required to extract DNA.

The DNA extracted when compared, extremely faint band was seen with single whitefly samples (Figure 29U). Only through DNeasy tissue kit method good quality DNA was obtained with single whitefly.

- c) **Elution Buffer:** Volume of the elution buffer AE was very important in the extraction. It was found that when DNA in the column was eluted with 200 μ l of AE, the DNA was quite diluted, and yield was not obtained when electrophoresed. If the elution volume is reduced to 100 μ l there was considerable loss of DNA. Therefore, the DNA bound to the column was eluted only once with 50 μ l of AE buffer (Figure 29V).
- d) **DNA Yield:** DNA extracted from 10, 8, 5, 2 and single whitefly when electrophoresed, bands were obtained with 10, 8 and 5 whiteflies, while it was not the case with 2 and 1 whitefly individuals. Data revealed that by the method standardized with resin column (Qiagen) (Table A). The ratio between absorption at 260nm and 280nm was more than one, indicating that the DNA did not have any protein contamination.

Table A Spectrophotometric estimation of yield of DNA

Brinjal (μ g/5 μ l)	Cotton (μ g /5 μ l)	Okra (μ g /5 μ l)	Soybean (μ g /5 μ l)
0.8	0.7	0.55	1.72

The above observations indicate that a single genomic DNA band at a position equivalent to 22 kb (Figure 29T) with intense fluorescence without shearing which can be considered as qualitatively good DNA was obtained only in the method using DNeasy tissue kit, with the conditions standardized as given above.

4.2.2. Optimization of PCR

It was necessary to optimize the PCR conditions, to evolve the protocol that will yield a consistent PCR pattern for the given DNA. Following parameters were evaluated by changing at a time only single parameters. In these studies, the DNA template used was obtained from the cotton population and the primers used were E4 and F2.

- a) **Quantity of DNA template:** 20, 40, 60, 80, 100 and 200 ng of DNA were subjected to PCR to find out the minimum concentration of DNA required. PCR details are as given in Material and Methods. ~10-15ng of DNA gave rise to good recognizable amplicons. Less than 10 ng of DNA no amplicon was obtained. In reactions employing 100, 200ng of DNA, sheared DNA distributed throughout the lanes was observed.
- b) **Magnesium Chloride concentration:** Concentration of 1.5mM, 2.0mM, 2.5mM, 3.0mM and 3.5mM were evaluated for clarity of bands. PCR products, were faint or absent at 1.5mM, 2.0mM and 2.5mM, while 3.0mM and 3.5mM gave distinct amplicons. Best results were obtained with 3.5mM as it showed intense fluorescence.
- c) **Annealing temperature:** Annealing conditions were standardized for operon primers, namely A-E (E4) and F2, F12, H9, H16; and temperatures of 35⁰C, 37⁰C, 38⁰C (for A-E) and 36⁰C, 37⁰C, 40⁰C (for F2, F12, H9, H16) were evaluated. Results showed that annealing at 38⁰C was optimum for A-E series primers and annealing at 40⁰C was suitable for F2, F12, H9 and H16 primers.
- d) **PCR Profile and number of cycles:** Three PCR profiles evaluated are given in Table B. The profile 3 with initial denaturation of 94⁰C for 2min., annealing at 38⁰C for A-E series and 40⁰C for F2, F12, H9 and H16 primers gave good amplicons. These conditions were adapted to generate the PCR patterns for the studies. (Figure 29W)

Table B Optimization of PCR protocols

Optimization details	Profile 1	Profile 2	Profile 3
	Temperature in °C for Time in min.	Temperature in °C for Time in min.	Temperature in °C for Time in min.
Initial Denaturation	94 for 2	94 for 2	94 for 2
Denaturation	94 for 1	94 for 1	94 for 1
Annealing	35/36/37/38/40 for 2	35/36/37/38/40 for 1.25	35/36/37/38/40 for 2
Extension	72 for 3	72 for 1.50	72 for 2
Final Extension	72 for 10	72 for 5	72 for 10
No. of cycles	30	34	40

4.2.3. Analysis of PCR profiles

The PCR conditions standardized were employed for generating PCR profile from the genomic DNA extracted from single whitefly. Amplification was repeated thrice and the amplicon obtained at least in two experiments was considered to represent the PCR product. Size estimates were approximated and assessed in comparison with the 1kb molecular weight marker (MBI Fermentas). Wherever amplicon is on par with two bands of molecular weight markers, arbitrarily they were assigned size. The results obtained are summarized below.

a) **Primers giving PCR products:** A total of one hundred four primers consisting of A-E series and F2, F12, H9 and H16 (reported by deBarro and Driver 1997 as giving polymorphism in *B. tabaci*) were evaluated. Forty-one primers gave amplification products (Table 81); a great majority did not yield any results (Table 82). Results revealed that F2, F12 and H16 were the only primers that amplified DNA from all the four populations, while thirty-three primers from A-E series amplified only one each of the populations. It was significant that the amplifications obtained with forty-one primers were highly specific. Thirty-three primers amplified only one population. For example, the primers C4, D5, and B5 amplified only DNA from okra population and not others.

Perusal of data on amplification of okra population showed that while some primers (B5, D6, D8, E13 and C10) gave rise to only single product, few others (A12, C4, C18, D19, D5, E5 and E8) gave rise to polymorphic products. In the case of brinjal population only four primers (D18, D7 and E9) gave rise to specific products, and the other primers gave varying products (A11, A14, A16, A10 and B19). Results with cotton populations were unexpected in the respect that the number of primers that yielded PCR amplicons was very few. In the case of soybean population, two primers (D13 and E20) gave single PCR products and five primers gave polymorphic pattern (A6, A9 and C5). The detailed results are as follows:

b) Primers amplifying only single population: Of the forty one primers that yielded PCR amplicons, thirty three primers amplified DNA from only one population. Among them maximum number of primers (12) amplified okra DNA; amplicon ~ 750bp was seen frequently, than other products. Brinjal population could be amplified with a maximum of ten primers, soybean with six and cotton with five primers. Primers were thus very specific in differentiating populations and could be considered as differentiating primers (Fig. 29A-L; Table 83).

c) Primers amplifying two populations: B12, D15 and E4 primers were found to amplify two populations each. B12 amplified brinjal and soybean and E4 each okra and soybean; however, the amplicons were different, it was 500bp, 750bp in case of brinjal with B12 while it was 500bp, 750bp, 1000bp and 1500 bp in case of soybean population. D15 was also observed to amplify brinjal and gave amplicons of 750bp, 1000bp and 2000bp and with okra at 2000 bp. (Fig. 29M-O; Table 84).

d) Primers amplifying three populations: A13 is the only primer in A-E series to provide amplification in the three populations viz. brinjal, cotton and soybean. Unexpectedly the okra population, which was amplified by highest number of primers

(12) was not amplified by this primer. The products of amplification with this were varying; amplicon ~750bp and ~1000bp were seen with cotton and brinjal, while soybean showed different profile. H9 amplified in case of brinjal, okra and soybean. (Fig. 29P,S; Table 85).

e) **Primers amplifying four populations:** The primers F2, F12 and H16 amplified all the four populations and it was interesting to observe that F2 and F12 giving rise to similar products 650bp and 750bp. These primers also gave rise to differentiating polymorphic products. The amplification with H16 clearly gave an indication of polymorphism occurring among the populations. Except for the ~ 1000bp products common to okra and soybean, all the other products were highly distinct and specific (Fig. 29Q,R,S; Table 86).

f) **Identification of polymorphic primers:** Compilation of all the PCR products with different primers was done to identify the primers that will indicate the extent of polymorphism. As Table 85 indicates, the primer A-13 and H9 that amplified three populations, primers F2, F12 and H16 that differentiated all the four populations were selected as important markers that will give good indications of polymorphism. The polymorphic products obtained are distinct and specific for each combination.

g) **Genetic similarity analysis of the phenotype:** The genetic similarity between the four populations from brinjal, cotton, okra and soybean differing in their RAPD-PCR phenotype was calculated using UPGMA and is given in the dendrogram (Fig.30). The analysis clearly indicates that brinjal population is very distinct and has less percentage of sharing its PCR products with other populations. Genetic relatedness between cotton and okra populations are higher than that with soybean; therefore, soybean population branches off separately and cotton, okra populations cluster together.

4.3. Transmission Studies

Inoculation of 7 days old soybean (cultivar Pusa 16) and mungbean (cultivar TS16) seedlings (Fig. 31-2A, 3A) were done with a single whitefly from the four populations studied. However, to confirm whether the population is capable of transmission at all, transmission was also done with 50 whiteflies. For each transmission study four replications were maintained (Fig. 31-2B, 3B). Single whitefly in an eppendorf tube was allowed to feed on *Mung Bean Yellow Mosaic India* virus (MYMIV) infected soybean seedlings for 24h (acquisition access period) and they were released on 7 days old healthy seedlings in acrylic cages for 24 h (inoculation access period). After the inoculation plants were maintained in insect proof cages and observations recorded. DNA was extracted from the whitefly after acquisition access and amplified with primers specific for MYMIV (*vide* Material and Methods). Plants were periodically observed for appearance of symptoms. DNA was extracted from the first trifoliate leaf of the inoculated seedlings to detect the viral DNA. (Fig.31-4).

- a) **Detection of viral DNA in the whitefly population:** Amplification with viral specific primer gave ~400bp (Open reading frame of transcription activator protein ORF AC2) product in all the four populations studied; no difference was observed indicating that the populations acquire the virus efficiently.
- b) **Symptom production in inoculated seedlings:** The plants inoculated with single whitefly did not show any symptoms till 30 days, while inoculation with 50 whiteflies gave rise to 80-100% transmission and symptoms within 7-10 days (Fig. 31-5). PCR amplification of leaf extract with viral specific primer of those plants inoculated with single whitefly did not give rise to any amplicon in case of single whitefly transmission studies while, amplicons were seen in all the cases with 50 whiteflies confirming viral pathogenicity. (Fig. 31-2C, 3C,4).

The above observations indicate that all the four populations of *B. tabaci* are similar in their virus transmission characteristics, with a 24h each of acquisition access and inoculation access periods. These results confirm the similarity of the populations in their transmission characteristics and that these populations have similar co evolutionary relationships with the MYMIV. Indeed the results also reveal that single whitefly transmission of the disease has not been confirmed effectively with all the four populations studied.

Discussion

5.1. Morphometric studies

The interpretations obtained in the present study corroborated with the trends defined by David and Ananthakrishnan (1976) and Mohanty and Basu (1986; 1987) on the morphometrics of intraspecific populations of *B. tabaci*. The fourteen characters, which the former deployed and the various parameters used by the latter in the evaluation of phenotypic differences in the populations occurring in different host plants, supplemented the basis of the present study. The reviews and analyses presented by Zelditch *et al.*, (2004) on the geometric morphometrics of shape of objects helped the present study in many angles, in particular towards the multivariate analyses and their use in obtaining the results. Likewise the studies done by Sneath and Soakal (1973), Cornuet and Louveaux (1981), Kshirsagar (1983), Ramakrishnan (1983), Byrne and Houck (1990), Bethke *et al.* (1991), Bellows *et al.* (1994), Bedford *et al.* (1994), Bryant and Meffert (1995), Fishpool *et al.* (1995), Gergis and Adam (1996), Chen (1997), Anez *et al.* (1997), Gaur *et al.* (1999, 2000a, 2000b, 2001), Shima *et al.* (2000), Kalaisekar (2003), Bustamente *et al.* (2004) and Klimov *et al.* (2004) provided the backdrop and the necessary background for the morphometric studies.

The intraspecific populations of *B. tabaci* occurring in the brinjal, cotton, okra and soybean agroecosystems of Delhi showed statistically significant variations in the important morphometric characters in the puparia and adults. In depth analysis of morphometrics of taxonomic characters attempted in the study led to important findings of significance to the taxonomy. These results indicate the possibility of distinguishing these populations as distinct taxonomic entities taking into account these characters showing statistical significance. The studies on the coefficient of variation have led to the

selection of stable characters for their distinction. The analyses of least square differences of the means have led to findings of importance to characterize the means of different characters and their variation. The correlation studies have brought out the nature of relationships between these characters and in a limited manner have indicated their distinction as taxonomic entities. The multivariate analyses involving MANOVA, principal component analysis and discriminant function analysis have revealed the relationships between the different populations and the causes and effects of the different morphometric variations. The salient results and their implications are discussed below.

There are 77 morphometric characters of the puparia 24 relating to dorsal setae, 16 relating to abdomen, 7 in transverse median suture, 6 in the vasiform orifice, 4 each in whole puparia, tracheal fold, caudal furrow, operculum, lingula and 3 in the caudal setae which were considered, of which many did not show consistency/ amenability for measurement or analyses. Among the ones that showed fitness and amenability for analysis, 16 characters belong to those of abdomen, 5 of vasiform orifice, 4 each of whole puparia, caudal furrow, operculum and lingula, and two characters to that of caudal seta. These indicate that whole of transverse median suture and tracheal fold have no relevance whatsoever in distinguishing the populations or defining the intraspecific populations at least in brinjal, cotton, okra and soybean. One can easily ignore these characters while describing the species of *B. tabaci* and other species, which are related to it. Usually it is indicated that the tracheal fold and transverse suture will have a number of taxonomically significant relationships in the puparia of whiteflies but in the case of *B. tabaci*, there are no variations in these, which are fit enough to be used as taxonomic characters. Possibly, transverse suture and tracheal fold have no role to play in the evolution of the species complexes in *Bemisia*. In most cases, it is the dimension of breadth, which has more relevance to statistical significance, for e.g., 11 characters of the G14 and 13 of the

G21+G2, amounting to a total of 24 characters had been found to be significant in their breadth, when compared to only 12 of those concerned with the dimension of length. Thus it could be seen that many of the taxonomic characters in terms of length, except those of different abdominal segments, have undergone plasticity and achieved stability in *B. tabaci*. In spite of significant variations in the populations, there are no associated differences in terms of length, when compared to that of breadth. All these indicate except lingula, caudal furrow, operculum, puparia as a whole, and those of abdominal segments 2,1,3,5,4,6,7 and 8, one need not give any importance to the measurements in terms of length for the distinction of the populations. These also point towards the fact that taxonomic descriptions need not take into account at all, the tracheal fold and transverse suture, but instead focus on other aspects namely caudal furrow, lingula, and abdominal segments, so that differences can be made more explicit for the purpose of authentic identification.

There had been taxonomic descriptions leading to establishment of new species like *B. pongamiae* Takahashi and *B. moringae* David and Subramaniam or defining *Bemisia* as a distinct genus (Jesudasan and David, 1991) highlighting the variations in the tracheal fold and transverse suture. But the present study has proved to the contrary and revealed that such details could be easily ignored. While we can conclude that these characters have no significant connotation to the distinction of the genus, species and intraspecific populations, they do have other meanings. That is, in spite of varied populations, these characters do not differ in the species within and therefore will be quite valuable in diagnosing the species *per se* that is *B. tabaci* in concrete terms. We can prescribe now characters based on statistical significance and consistency in an accurate manner than before.

There had been instances in the whiteflies' taxonomy where undue emphasis had been laid on the caudal or dorsal setae, as these are the only visible and contrasting aspects of abdomen without taking any measurements. The present study makes it known categorically that such reliance on the setae will be faulty and rather misleading. In particular, the numbers of dorsal setae are not at all reliable, and it is also subjected to variations due to even slight difference in the host phenotypes like hairy or glabrous nature. When the specimen is dried and preserved, it is also possible that these structures, which are flimsy, get dislodged. There is a need to give more importance to these aspects of abdomen, the study reveals, if one wants to rely on the characters in the abdomen of whiteflies, in particular *B. tabaci*.

As far as the characters of *B. tabaci*, which show statistically significant variations, it could be seen that the abdomen with 15 measurements; vasiiform orifice and whole puparia with 5 measurements each; caudal furrow and operculum with 4 measurements each; lingula with 3 measurements; and caudal seta with 1 measurement are the major contributors of variations leading to the establishment of the populations from the four crops as distinct morphological and thereby taxonomic entities. The breadth and length aspects of different abdominal segments are the best bets to provide many measurements for the differentiation of the four populations. These characters tend to vary much due to the effect of the hosts and to such an effect that the four populations from brinjal, cotton, okra and soybean are distinct as different taxonomic entities.

If the analysis is focused for singling out characters enabling the distinction of these populations, it could be seen that the breadth of submargin of puparia is an extraordinary statistically significant one, as it is distinct with an F value of 481.95 at probability value of 3.57×10^{-85} ; it is simultaneously found to be consistent with its coefficient of variation (CV) of only 9.36 percent for all the populations. All other

characters in the G14 group though likewise statistically significant at good levels of probabilities to distinguish the populations, need to be used with caution as their coefficient of variation are going at higher levels. The two characters of caudal furrow namely breadth at apex and base and that of abdominal segment 8 which fall under this group bear testimony to this statement as their CV values build to as high as more than 30 to 40 per cent. Of the extraordinary statistically significant characters, the breadth of caudal seta, that of caudal furrow at middle, that of operculum at apex, vasiform orifice near base, abdominal segment 3, length of lingula, that of caudal furrow, breadth of puparia at middle, length of operculum, and breadth of abdominal segment 1 are the most important ones as all these showed the least coefficient of variation indicating the promise these hold for the separation of populations from the four crops as distinct taxonomic entities. These are reliable, consistent and stable characters with extreme variations among the four populations.

The breadth of submargin of puparia varies from 4.53 to 9.67 in the four populations in terms of indices. If we work out the breadth of submargin, it could be seen that population from soybean has the least length followed by population from cotton (mean= 6.58), okra (mean= 7.02), and maximum in brinjal (mean=9.67). These values indicate that the breadth of submargin of puparia has a better discriminatory potential in addition to having least C.V., indicating its superiority and consistency in differentiating the populations.

As far as the adults of *B. tabaci* are concerned, for analyzing the intraspecific variations, the following details could be obtained. The characters of the length and breadth of head, thorax, abdomen; and length of compound eye and proboscis are statistically significant in terms of F values and their coefficient of variation ranges

between 9.64 and 25.02, indicating that these characters are valuable in distinguishing the adults from the four different crops.

The morphometric studies had revealed that among the 37 characters, which had shown statistically significant variations, 34 characters had a CV value ranging between 8.06 and 18.23, while three characters had the same in between 30.35 and 42.95 per cent. The analysis of these statistics provided the basis for the identification of characters with great stability and these could be employed safely for the separation of the populations. Part of these results is in conformity with the conclusions obtained by David and Ananthakrishnan (1976), Mohanty and Basu (1986; 1987), Byrne and Houck (1990), Bethke *et al.*, (1991) and Chen (1997). The characters in their order of importance as concluded by the present study are given below:

1. Breadth of submargin
2. Breadth of caudal seta
3. Breadth of caudal furrow at middle
4. Breadth of operculum at apex
5. Breadth of vasiform orifice near base
6. Breadth of abdominal segment 3
7. Length of lingula
8. Length of caudal furrow
9. Breadth of puparia at middle
10. Length of operculum
11. Breadth of abdominal segment 1
12. Breadth of vasiform orifice at apex
13. Breadth of puparia at base
14. Breadth of lingula at middle

15. Breadth of operculum at base
16. Breadth of abdominal segment 2
17. Breadth of puparia at apex
18. Length of abdominal segment 2
19. Length of abdominal segment 1
20. Length of puparia
21. Length of abdominal segment 3
22. Length of abdominal segment 5
23. Breadth of operculum at middle
24. Breadth of vasiform orifice near apex
25. Length of abdominal segment 4
26. Length of abdominal segment 6
27. Breadth of abdominal segment 4
28. Length of abdominal segment 7
29. Breadth of abdominal segment 5
30. Breadth of vasiform orifice at base
31. Length of abdominal segment 8
32. Breadth of lingula at base

However, the following characters are to be deployed cautiously,

1. Breadth of abdominal segment 6
2. Length of vasiform orifice
3. Length of caudal furrow at apex
4. Length of caudal furrow at base
5. Breadth of abdominal segment 8

The interpretations taking into account the extent of relationship between the different characters qualified by simple correlation coefficients indicate that the morphometric behaviour of the populations from brinjal and okra is quite different. The evolution of characters and their relationships in terms of taxonomic values indicate that populations from cotton and soybean stand out as unique populations fit to be placed as distinct evolutionary units. Of the 562 negative correlations 441 are confined to the populations from cotton and soybean. It has also been shown that the characters in the abdomen including those of the caudal furrow, operculum, lingula and vasiform orifice are more significant in affecting the relationships. It is necessary that all these facts are to be given due consideration while undertaking the distinction of four populations as distinct taxonomic entities.

The perusal of literature indicated that though one can find out the statistical significance of variations in the taxonomic characters between the populations through single factor ANOVA, if one wants to cluster the samples, it is essential to proceed further with multivariate analyses. It could also be seen that whatever studies had been done so far in India (David and Ananthakrishnan, 1976; Mohanty and Basu, 1986; 1987) Kshirsagar, 1983; Gaur, 1998; Gaur *et al.*, 1999, 2000a, 2000b, 2001) had not taken this aspect into account and an attempt was made towards separating the four intraspecific populations of *B. tabaci*. The recent papers published by Bustamante *et al.* (2004) and Klimov *et al.* (2004) on the separation of populations using multivariate analyses like Principal Component Analysis (PCA), Multivariate Analysis of Variance (MANOVA) and Discriminant Function Analysis (DFA) provided the necessary impetus for the present study with regard to the multivariate analyses.

In the present study PCA was used to investigate morphological variations between the four populations of *B. tabaci* by involving 35 highly significant characters, which were identified by one-way univariate ANOVA. Using PCA, the dimensionality of the problem was reduced from 35 variables to five principal components. It could be seen that the first PC could explain more than 40 per cent of the variation and it was possible to narrow down to five variables by this analysis. Further, the plot of the PCs clearly separated the four populations without much overlapping. Thus the PCA could explore the differences among populations and identify the important sources of variations, which are associated with puparia. The MANOVA of these PCs showed significant variations between the populations. The DFA are useful for assessing the utility of the characters and for separating the populations in question. In the current study DFA could correctly classify 100 per cent of populations from brinjal, cotton, okra and soybean. A similar study conducted by other workers concluded that the DFA could identify correctly 71 per cent of a population and 76 per cent of another population and rated these percentages of classification as very supportive. In the light of this rating, the results of the present study can well be rated as highly supportive in separating the populations to a precision of 100 per cent. Further the plot of the two canonical discriminant functions clearly separated the four populations. Thus it could be concluded that the four populations of *B. tabaci* are in the process of evolving into different morphological and thus into distinct taxonomic entities, at least, while taking into account the characters of the puparia.

Likewise in the case of adults, such analyses of PCA and DFA had shown that first PC alone could explain 38 per cent of the variation and the first three PCs take care of more than 68 per cent of the variation in the four populations. The DFA observed that error rates were found to be higher than those found for the characters of the puparia,

indicating that the variations in the characters of the puparia are the best indicators. These could also be utilized to interpret that the puparia rather than adults are the best discriminatory stages for the distinction of the intraspecific populations of *B. tabaci*.

5.2. Molecular studies

The taxonomic distinction of *B. tabaci* is extremely difficult to achieve based on morphological characters alone, in view of its complex intraspecific populations, and its ability to produce variations in many of its established taxonomic characters. The insect has wide host range and depending on the host colonized, and physiological status of the host plant, key morphological characters vary (Mound, 1963). Variability in host range, virus transmission, fecundity, sexual compatibility, development rates, parasitoids and insecticide resistance are some of the parameters, which were used to differentiate its populations, as could be seen from the literature (Wool *et al.*, 1993, Wool *et al.*, 1994, Coats *et al.*, 1999, Gunning *et al.*, 1995). Thus there is enough evidence to suggest that the present *B. tabaci* is a complex of distinct intraspecific populations or biotypes (Frohlich *et al.*, 1999).

Till 1997, such differentiation of *B. tabaci* populations heavily relied upon simple but inefficient morphometric and allozyme based techniques. There is severe constraint in these methods as amount of material required for carrying out the analysis is large; and reproducibility of results was impossible due to variation in the physiology of the host plants. Therefore, a technique that is based on inherent genetic information of the insect was indispensable, which gave birth to RAPD PCR markers for identification of insect populations (Caterino *et al.*, 2000). In the present study attempts were made to develop PCR markers that will help in differentiating the selected whitefly populations from India. The objective of the study was to obtain concordant and reproducible data, hence it was imminent to standardize the protocols for the extraction of genomic DNA and optimize

the PCR conditions, in addition to conducting an analysis using the random primers available. The study achieved a protocol that will yield good quality PCR compatible DNA from a single whitefly; optimized PCR protocol/ profile to identify the PCR markers that will give good indication of polymorphism; and provided an analysis leading to dendrogram of the four populations selected for the study obtained from brinjal, cotton, okra and soybean.

DNA Extraction protocol: Perusal of literature show several DNA extraction protocols claiming to yield good quality DNA.(Dellaporta *et al.*, 1983; Doyle and Doyle, 1987; Lodhi *et al.*, 1994; Guirao *et al.*, 1997; deBarro and Driver, 1997; deOliveira *et al.*, 2000, Lima *et al.*, 2000 and Moya *et al.*, 2000). Unexpectedly, many of these procedures outlined in Dellaporta *et al.*, (1983), Doyle and Doyle (1987) and deBarro and Driver (1997) did not give quality DNA under our laboratory conditions. Often DNA concentration was extremely low and even if it was visible it was not PCR compatible. After comparison of all the methods, only the method using DNeasy tissue kit was observed to yield good results. It is inferred that the nitro cellulose membrane column provided in the kit perhaps effectively removes the inhibitory phenolic and tannin substances in the extract and helps in obtaining good quality DNA. However, the yield of DNA from single insect is very low ~ 1.2 ng/ul. Considering the importance of data generated from single whitefly, DNA extracted from single whitefly was used in all instances. Even though the kit required 50mg of insect, single insect weighing 2mg gave adequate quality of DNA.

Optimization of PCR: PCR conditions optimized focused towards the quantity of DNA template, MgCl₂ concentration, annealing temperature profile and number of cycles. It was found out that clarity of banding was ideal at an annealing temperature of 38°C for A-E primers, 40°C for F2, F12, H9 and H16. The melting temperature (T_m) for primer A-

E was 36°C and for primer F2, F12, H9 and H16 it is 39.5°C (Qiagen). Due to such configuration of melting profile, better annealing of the primer with template was possible at 38°C and 40°C. deBarro and Driver (1997) suggested that for F2, F12, H9 and H16 annealing at 40°C, while normally RAPD profiles are generated at 37°C, which supplements the results of the present study.

MgCl₂ concentration is an essential parameter of any PCR reaction (Ausubel *et al.*, 2001). In the present study MgCl₂ concentration of 3.5mM was found to be suitable for most primers. Attempts were made in the present study to generate RAPD profiles using one hundred and four primers for the four white fly populations selected. The primers A-E series were chosen randomly, besides F2, F12, H9, H16 chosen by deBarro and Driver 1997. The results of amplification with A–E series were very significant; 63 primers did not amplify the genomic DNA; it is considered that with these primers the amplification would have been very low, that they were invisible through gel electrophoresis. Previous workers had experienced absence of amplification with large number of primers and it is nothing new (Moya *et al.*, 2000, Lima *et al.*, 2000).

Of the 41 primers, which yielded results, more than thirty-three primers were highly specific, as these frequently amplified the DNA from only one population. For example the primer A12 gave results with only okra populations giving amplicons in the range of 550bp and 800bp, while the primers B5, C10, C18, D6, D8 and E13 gave single products in the range of 750bp, 750bp, 750bp, 1250bp, 750bp and 1000bp, respectively.

The extreme specificity is interesting, and it requires further validation with individuals collected from a specific isolate from different geographic regions. Further sequencing of the molecular marker, converting them to SCAR marker will lead to basis of genetic diversity. These primers if validated can be exclusively used to differentiate the populations. The primers F2, F12, H9 and H 16 were earlier shown to be useful in

Studying the polymorphism among different populations of whitefly (deBarro and Driver, 1997; deBarro and Driver 1998). The products obtained in the present study were compared with the results given by deBarro and Driver (1997). The population from India studied by him has given PCR products varying in size from 750bp, 1000bp, 1500bp and 2500bp while for the same primer the products obtained in our study were 500bp, 650bp, 950bp for brinjal, 500bp, 650bp, 750bp for cotton, 300bp, 500bp, 650bp, 750bp, 1000bp for okra and 500bp, 650bp, 750bp and 1000bp for soybean. While, there is similarity to some degree, there is enough diverse product profiles indicating the heterogeneity in the populations. Varying products seen in the four populations, though from the same geographical region indicated that genetic diversity. The similar bands obtained with the primer F12 for the whitefly population from brinjal (500, 650, 750), cotton (450, 750, 1250, 1500), okra (450, 600, 750, 1000, 1200) and soybean (500, 650, 750, 1000, 1200) however, may have to be viewed with caution. PCR product of the same size may represent pieces of different sequences, which can be understood only if nucleotide sequences are generated.

Application of molecular markers for differentiation of whitefly population is a recent development. (deBarro *et al.*, 2000; Frohlich *et al.*, 1999). Based on the phylogenetic analysis of mitochondrial cytochrome oxidase 1 gene, relationship between the populations from different geographical regions had been understood (Brown, 2000). It is suggested that while New World population showed a distinct lineage, Old World population could be differentiated into four or five groups, namely Group 1 Southeast Asia, Thailand, Malaysia and Pakistan; Group 2 originating from Mediterranean sea, including the biotype B; Group 3 from India, Pakistan, and Nepal; Group 4 Sub Saharan Africa. A substantial divergence was found to exist between the two subgroups present in the Indian subcontinent. The present study confirms the genetic diversity among

populations from brinjal, cotton, okra and soybean. There are many studies in which host related differentiation of biotypes in *B. tabaci* had been established recently. Cassava specific populations in the whitefly vector for Indian cassava mosaic virus and sweet potato biotype a non-vector of ICMV (Palaniswami *et al.*, 1996; Lisha *et al.*, 2003). The two host based biotypes are also different in their PCR profiles in addition to other characters. It will be rewarding to study the differences seen among the populations, whether transmission details would substantiate the molecular differences.

5.3. Transmission studies

Begomoviruses are transmitted exclusively by the whitefly, *B. tabaci* in a circulative persistent manner. This phenomenon of vector mediated transmission of viruses is expected to involve recognition between the viral capsid and whitefly vector receptor-like molecules that facilitate viral transport around the gut membrane and entry into the accessory salivary glands (Bridson *et al.*, 1990; Cicero and Webb, 1995; Rossell *et al.*, 1999; Ghanim *et al.*, 2001). Since there is a great interdependence between the virus and the vector, coevolution between the virus and vector is thought to operate as the major mechanism that will determine the transmission ability of the vector (Brown, 2000). For example the new world whitefly population will transmit new world begomoviruses more efficiently than the old world begomoviruses.

In the present study with MYMIV, all the four populations, though acquired the virus, single whitefly transmission could not effectively result in disease symptoms. The virus concentration introduced into the plant may be so small that its further replication and establishment was not achievable. However, the populations under study were efficient vectors was evident from 100 per cent per cent transmission obtained with fifty whiteflies. Reddy and Rao (1989) and Nair and Nene (1973) concluded that even a single whitefly can transmit the MYMIV after an acquisition access period and inoculation

access period of 24h infecting 25 per cent of the inoculated plants; however, for 100 per cent transmission efficiency to occur 4-10 whiteflies were required.

In the present study, all the four populations transmitted the MYMIV, indicating that though these are genetically diverse, they may not differ in their transmission properties, and all the four populations might be having an equally coevolving relationship with the virus. Presence of the virus in the vectors as detected by PCR revealed that the virus was ingested by all the four populations efficiently, even if virions could be delivered, the amount was not enough to result in pathogenesis.

Summary

The whitefly *Bemisia tabaci* is one of the most injurious whiteflies, not only due to its plant sap sucking nature but also due to its virus transmission capabilities, which magnify its role as a vector. Of late *B. tabaci* is gaining importance in agricultural and horticultural crops due to its complex intraspecific populations and biotypes, which are differentiated by various cumbersome characteristics. Detailed studies for exploring the morphometrics of puparia and adults of *B. tabaci* and coupling these with molecular and transmission studies for interpretations of biosystematic significance are lacking, in particular in India. Hence, with this background in mind studies were undertaken on the populations of *B. tabaci* obtained from brinjal, cotton, okra and soybean at Delhi and the salient findings are summarized below.

- A total of 77 characters were taken up for morphometric studies on the puparia of *B. tabaci* and it was observed that many of these characters are neither uniform, stable, consistent nor amenable for measurement. Studies on the host related morphological or phenotypic variations shall take cognizance of this fact and shall proceed only after further confirming these details on the various populations.
- Out of the 39 characters subjected to one-way single factor ANOVA for their statistical significance in differentiating the populations it was observed that 37 characters showed significant variations between the four populations of *B. tabaci* in terms of F values, at the probability levels above 0.01 and 0.05.
- There are two non-significant characters namely the breadth of abdominal segment 7 and that of lingula. It can be seen that both these are on the dimension of breadth alone and mainly belong to the abdominal segment 7 and lingula. Of these two, the character of breadth of lingula at base can be considered marginally distinct, as it is

significant at the probability level of 0.07 and must be considered with caution as far as future studies on morphometrics of populations is concerned.

- As far as the significant characters are concerned, the statistical analyses indicate that these populations are quite different from each other, and the deviation between the populations with respect to these characters is drastic, thereby signalling that the populations from brinjal, cotton, okra and soybean are transforming into morphologically and taxonomically distinct entities.
- These are characters that show significant variations, between the populations, at the probability levels of 2.14×10^{-11} and above. In statistical terms these have extraordinarily high level of significance as the F values of their variations fall between 20.58 and 481.95, which are much higher than their critical F values. Hence, these characters can be considered as very highly significant and important for the distinction of the populations morphologically.
- There are six characters namely, breadth of submargin; breadth of caudal setae; breadth of caudal furrow at the middle, at apex, and at base; and breadth of abdominal segment 8 stand out due to their statistical significance at extremely high levels of probability namely, 3.57×10^{-85} (F value 481.95), 9.26×10^{-67} (F value 335.06), 2.04×10^{-32} (F value 81.34), 7.5×10^{-28} (F value 65.01), 3.15×10^{-26} (F value 59.98) and 9.3×10^{-22} (F value 46.57), respectively. These probability levels, according to the statistical parlance are very highly significant, resulting in the calculated F value soaring much higher than the critical F value.
- As far as the caudal furrow is concerned the breadth at middle is more important as it is showing variations at a high level of significance with an F value of 81.34 significant at a probability level of 2.04×10^{-32} . The breadth at apex and at base are

relatively less superior in discriminating the populations; their significance being at probability levels of 7.5×10^{-28} and 3.15×10^{-26} , respectively

- The breadth of abdominal segment 8 is the other character to fall in line with the above, with its significance being at the probability level of 9.3×10^{-22} . These results also indicate that soybean had profound effect on the breadth of caudal furrow effecting significant taxonomic variations.
- There are twenty-one characters, which show statistical significance at the probability levels between 1.41×10^{-10} and 6.01×10^{-4} with their F values ranging between 19.09 and 6.06. Among these are ten characters from the abdominal segments namely, breadth of abdominal segment 2, 4, 5 and length of abdominal segments 1, 3, 5, 4, 6, 7, 8. Also, among these are characters located on the vasiform orifice (3), lingula (2), operculum (2), besides breadth at apex and length of puparia as a whole. If we consider these characters as a whole, it is evident that the maximum numbers of these characters are on the abdomen, which indicates that to distinguish the populations, importance must be given to the study of characters on the abdomen. This also emphasizes the fact that morphometrics in terms of the dimension of breadth is more important than length in case of many characters that are taxonomically important in puparia.
- The one way single factor ANOVA carried out with regard to the ratios between the selected characters indicate that except for the dimension of length vs. breadth of puparia, all other ratios between the different body parts are significantly different for the four populations. These results also indicate that the characters in the abdomen play a significant role in morphometrics of puparia of *B. tabaci* and in differentiating the four populations.

- 24 characters taken up for morphometric studies on the adults of *B. tabaci* many of these are neither uniform, stable, consistent nor amenable for measurement. These observations indicate that, in spite of these characters being utilized by various whitefly taxonomists for defining *B. tabaci*, these are not of morphometric significance and any study focused towards the host related morphological or phenotypic variations shall take cognizance of this fact and shall proceed only after further confirming these details on the various populations. These results also reveal that it will be advisable to refrain from using these characters in the definition of adults of *B. tabaci*; if at all it is indispensable to use them it must be used with caution.
- Out of the 10 characters of adults subjected to one-way single factor ANOVA for their statistical significance in differentiating the populations it was observed that 8 characters showed significant variations between the four populations of *B. tabaci* in terms of F values, at the probability levels above 0.01 and 0.05.
- There are two non-significant characters namely breadth of compound eye and that of proboscis. Thus it can be seen that both these are on the dimension of breadth alone and the probability levels at which these characters can turn significant vary between 0.07 and 0.47, indicating their absolute invalidity in defining the populations as morphologically distinct units. These results reveal that though these characters can turn out to be important in the event of utilizing the taxonomic and morphological aspects of adults of *B. tabaci*, and other related whiteflies, when turned into measurements and analyzed for morphometrics have no significance in distinguishing the populations occurring on the four crops.
- The analysis of the eight significant characters indicates that the populations from brinjal, cotton, okra and soybean are quite different from each other, and the deviation

between the populations is drastic, thereby signaling that these populations are transforming into morphologically and taxonomically distinct entities

- It can be observed that the ratios between the length and breadth of proboscis in adults provides the most significant dimension (at probability level of 1.6×10^{-120} and F value of 1108.6) which could be exploited to distinguish the four populations of *B tabaci* occurring in brinjal, cotton, okra and soybean.
- The coefficient of variation for the 37 characters found significant in the puparia ranged from a minimum of 8.06 per cent for the breadth of vasiform orifice at base to a maximum of 42.95 per cent for the breadth of caudal furrow at base. These indicate that all the 37 characters that showed significant variations, in the ANOVA, between the four populations are not equally fit to be used as stable characters to distinguish the populations as distinct morphological and taxonomic entities.
- It could be seen that the breadth of submargin of puparia is a reliable, consistent and stable taxonomic character, which could be exploited for the separation of the populations from brinjal, cotton, okra and soybean as distinct morphological entities.
- The coefficient of variation for the eight characters of adults varied from a minimum of 9.26 per cent for the length of proboscis to a maximum of 21.11 per cent for the breadth of abdomen. These indicate that all the eight characters, which showed significant variations, in the ANOVA, between the four populations, are not equally fit enough to be used on par as stable characters to distinguish the populations as distinct morphological and taxonomical entities.
- There is one character, which exhibited variations within the individual populations to the extent of reaching the CV values of more than 20 per cent; it is the

breadth of abdomen , wherein the CV values for all the populations considered together reached 21.11 per cent.

- All these results indicate that these characters of the adults of *B. tabaci* are considerably and comparatively much variable and are to be used with caution in distinctly defining the four populations as taxonomic entities, though these are exhibiting significant variations in terms of F values over single factor ANOVA tests.
- There are six characters namely breadth of puparia at apex, of submargin that of caudal furrow at apex, length of operculum and breadth of vasiform orifice near base which have their means/least square mean values distinct from each other. These characters can be utilized to separate the four populations obtained from the crops namely brinjal, cotton, okra and soybean for distinguishing purposes. It will also be worthwhile to observe that except for the breadth of caudal furrow at apex, all other characters have their co-efficient of variation ranging between 9.36 and 13.71 when all the populations were considered together. All these indicate that these characters are unique with respect to their statistical significance in these variations persistent to a population of a specific host and are also consistent and persistent within them. From these it can be concluded that these characters can be safely identified for the distinction of the populations.
- There is no morphometric character in the case of adults which gets isolated in terms of least square differences of means over the four different populations from brinjal, cotton, okra and soybean, making their distinction amply evident. These observations indicate that the host related variations in definite morphological dimensions in adults are not to the same degree as seen in the case of puparia. It will be worthwhile to bank upon the morphological dimensions of puparia rather than adults for definite interpretations on the host related phenotypic variations in *B. tabaci*.

- There are 562 negative correlations in the relationships between the characters in the four crops, of which the majority of 441 are confined to the populations from cotton and soybean, indicating that the morphometric behaviour of these populations is quite different from the crops namely brinjal and okra. Of these, particularly the characters in the abdomen including those of the different abdominal segments and those of the caudal furrow, operculum, lingula and vasiform orifice had the majority of their relationships with each other negative, indicating that these are more significant in affecting the relationships between the characters and hence are very important in the phylogenetic analyses. These results also point to the fact that these morphometric relationships isolate populations from cotton and soybean as distinct taxonomic entities and hence the 37 characters significant through one way single factor ANOVA could be conveniently used to distinguish these populations as morphologically and taxonomically distinct units.
- In case of adults of *B. tabaci*, the populations obtained from brinjal and cotton had more number of their relationships (33 to 40 per cent) negatively correlated with each other. In contrast, the populations from okra and soybean had majority (88 to 95 per cent) of the relationships between morphometrics positively correlated with each other indicating that the host correlated phenotypic variations in the adults are entirely on a different note when compared to the puparia.
- Through MANOVA it could be observed that five PCs of the characters in the puparia show significant variations among the four populations obtained from brinjal, cotton, okra and soybean. These results also clearly indicate that the populations coming from these different crops show variations in the taxonomic characters considered in puparia for identification of *B. tabaci*. In the case of adults three PCs were able to show the significant variations among the four populations, and these could convincingly

conclude that the populations obtained from brinjal, cotton, okra and soybean are morphometrically different as in the case of puparia.

- Thus, based on all the statistical analysis, it can be concluded that there exists definite distinction between the populations coming from the four crops. The dendrogram of relationships between the four populations is depicted in Fig. 28, which shows that the brinjal and soybean populations are closer, and branch out from those of cotton and okra.
- Standardization of protocol for isolation of genomic DNA, optimization of various parameters for RAPD-PCR and analysis profiles of DNA was achieved through molecular studies on *B. tabaci*.
- Protocol to isolate RAPD-PCR compatible and good quality DNA was standardized after evaluating 2% Cetyl Trimethyl Ammonium Bromide (CTAB) Method, Modified 2% CTAB Method, Lysis buffer method and DNeasy tissue kit (Qiagen) ATL buffer, of which the later was found to be the efficient.
- Other protocol aspects namely lysis time, number of insect(s), elution buffer and DNA yield were evaluated for the extraction of DNA. With the protocols standardized, genomic DNA band at a position equivalent to 22 kb with intense fluorescence without shearing was obtained which can be considered as qualitatively good DNA.
- To optimize the PCR conditions and to evolve the protocol that will yield a consistent PCR pattern, quantity of DNA template, $MgCl_2$ concentration, annealing temperature, PCR profile and number of cycles were evaluated. ~10-15ng of DNA, 3.5mM $MgCl_2$, annealing at 38°C for A-E series primers and 40°C for F2, F12, H9 and H16 primers were optimized in generating the PCR profile. The profile evaluated with initial denaturation of 94°C for 2min., annealing at 38°C for A-E series and 40°C for F2, F12, H9 and H16 primers gave good amplicons. These conditions were adapted to generate the PCR patterns for the studies.

- A total of one hundred four primers consisting of A-E series and F2, F12, H9 and H16 were evaluated of which Forty-one primers gave amplification products a great majority did not yield any results.
- Results revealed that F2, F12 and H16 were the only primers that amplified DNA from all the four populations, while thirty-three primers from A-E series amplified only one each of the populations. It was significant that the amplifications obtained with forty-one primers were highly specific. Primer A-13 and H9 that amplified three populations, primers F2, F12 and H16 that differentiated all the four populations were selected as important markers that will give good indications of polymorphism.
- The genetic similarity between the four populations from brinjal, cotton, okra and soybean differing in their RAPD-PCR phenotype calculated using UPGMA indicates that brinjal population is very distinct and has less percentage of sharing its PCR products with other populations. Genetic relatedness between cotton and okra populations are higher than that with soybean; therefore, soybean population branches off separately and cotton, okra populations cluster together.
- The observations on virus transmission aspects with MYMIV indicate that all the four populations of *B. tabaci* are similar in their virus transmission characteristics, with a 24h each of acquisition access and inoculation access periods.
- These results confirm the similarity of the populations in their transmission characteristics and that these populations have similar co evolutionary relationships with the MYMIV. Indeed the results also reveal that single whitefly transmission of the disease has not been confirmed effectively with all the four populations studied.
- It can be concluded that the populations of *B. tabaci* occurring on brinjal, cotton, okra and soybean are taxonomically distinct. Further studies are required to cover more crops, more seasons and more geographical variations before coming out with valid interpretations on the biotypes of *B. tabaci* in India.

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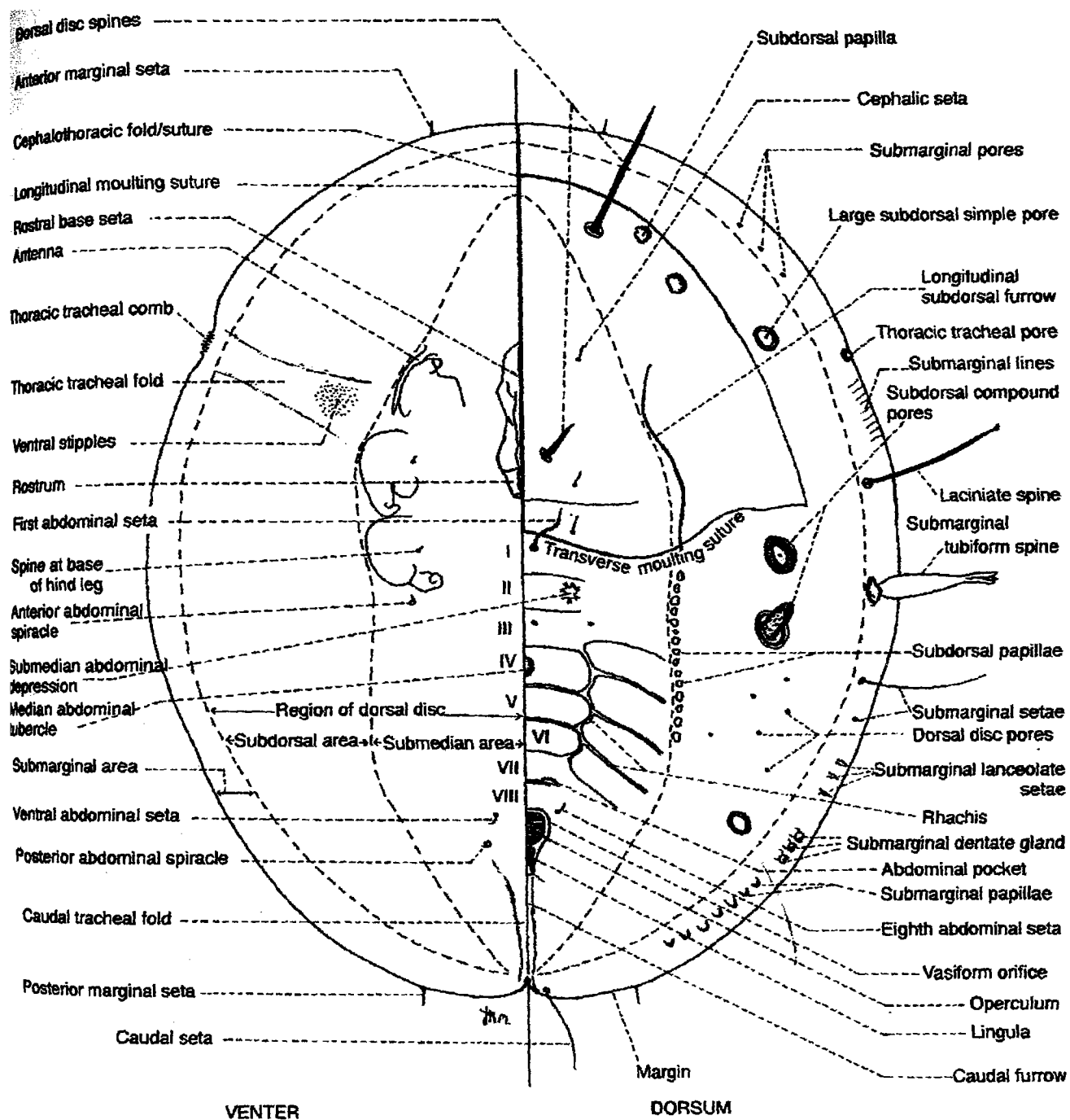


Fig. 1. Characters of *B. tabaci* in the puparia

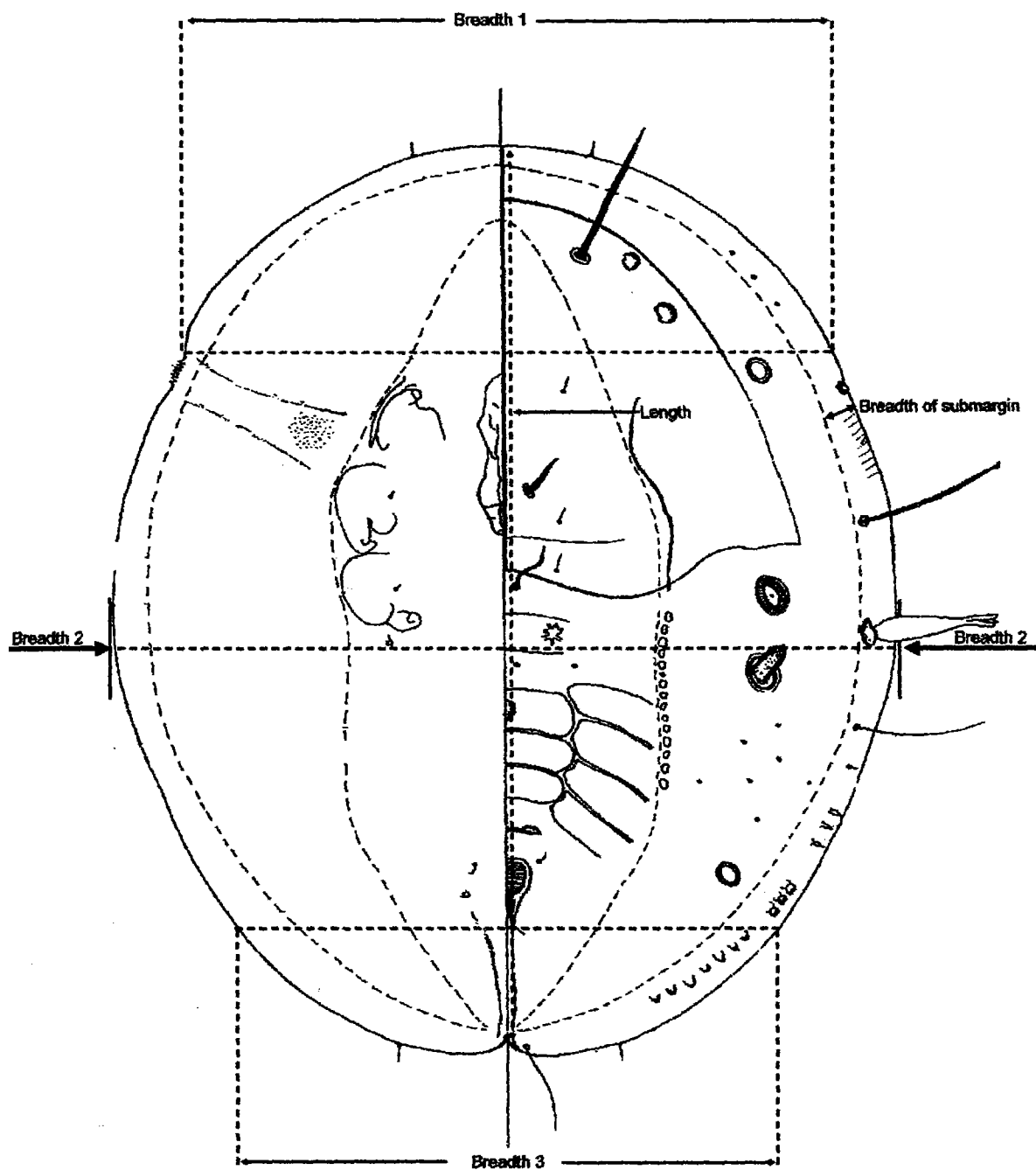


Fig. 2. Characters selected for morphometric studies in puparia

abdominal segments

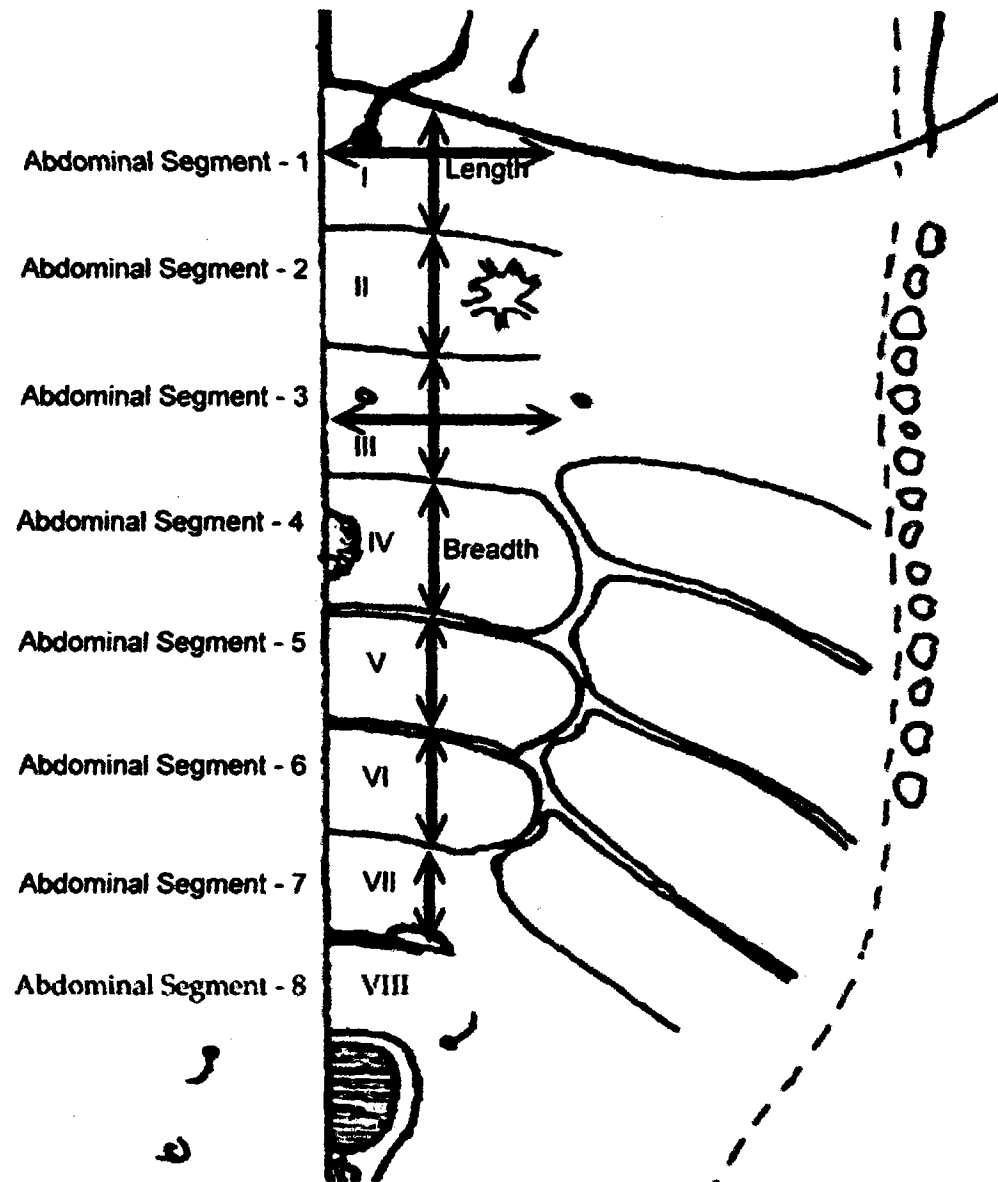


Fig. 3. Characters selected for morphometric studies in puparia - abdominal segments

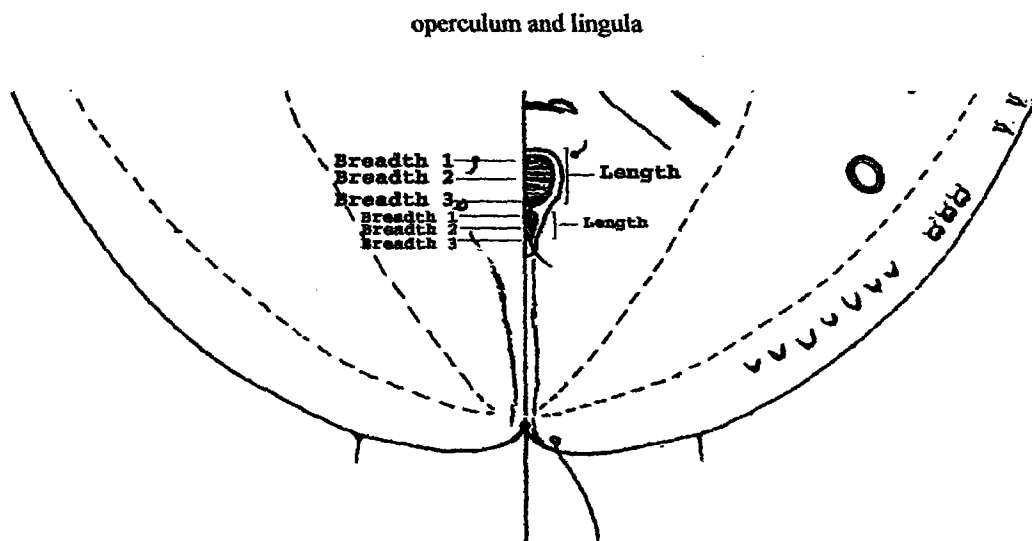


Fig. 4. Characters selected for morphometric studies in puparia - operculum and lingula

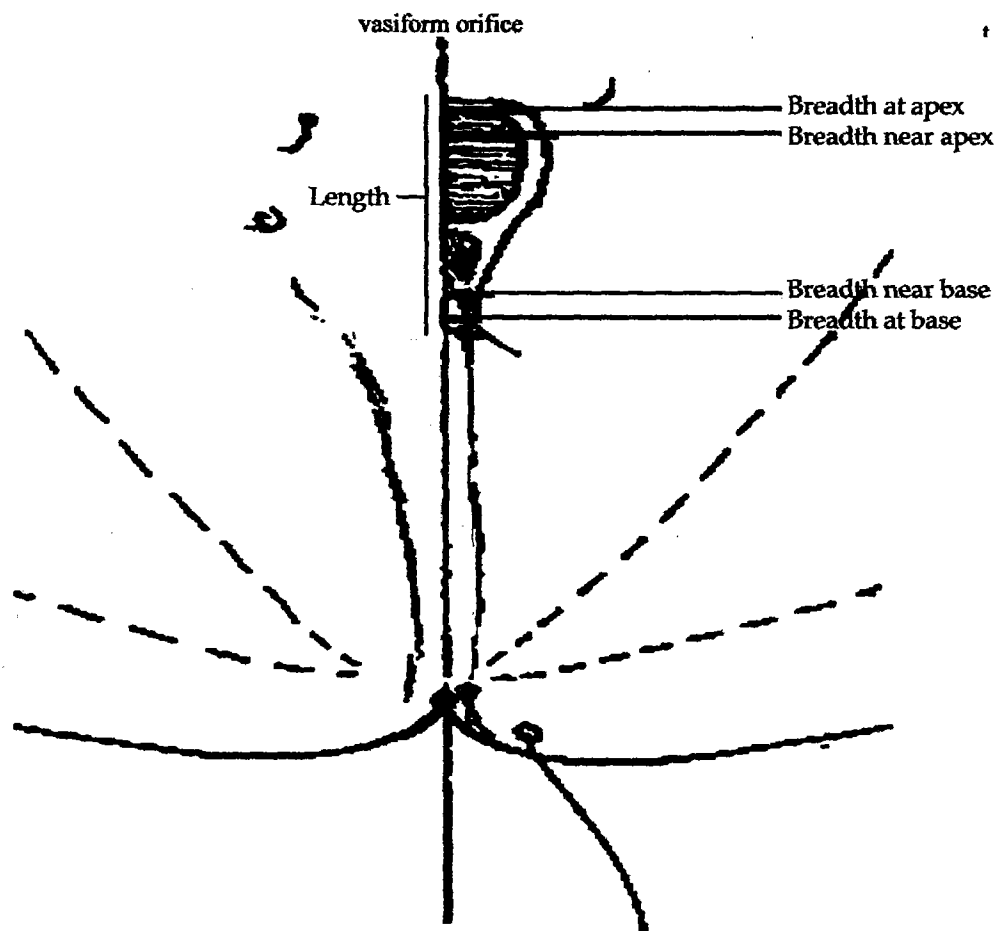


Fig. 5. Characters selected for morphometric studies in puparia - vasiform orifice

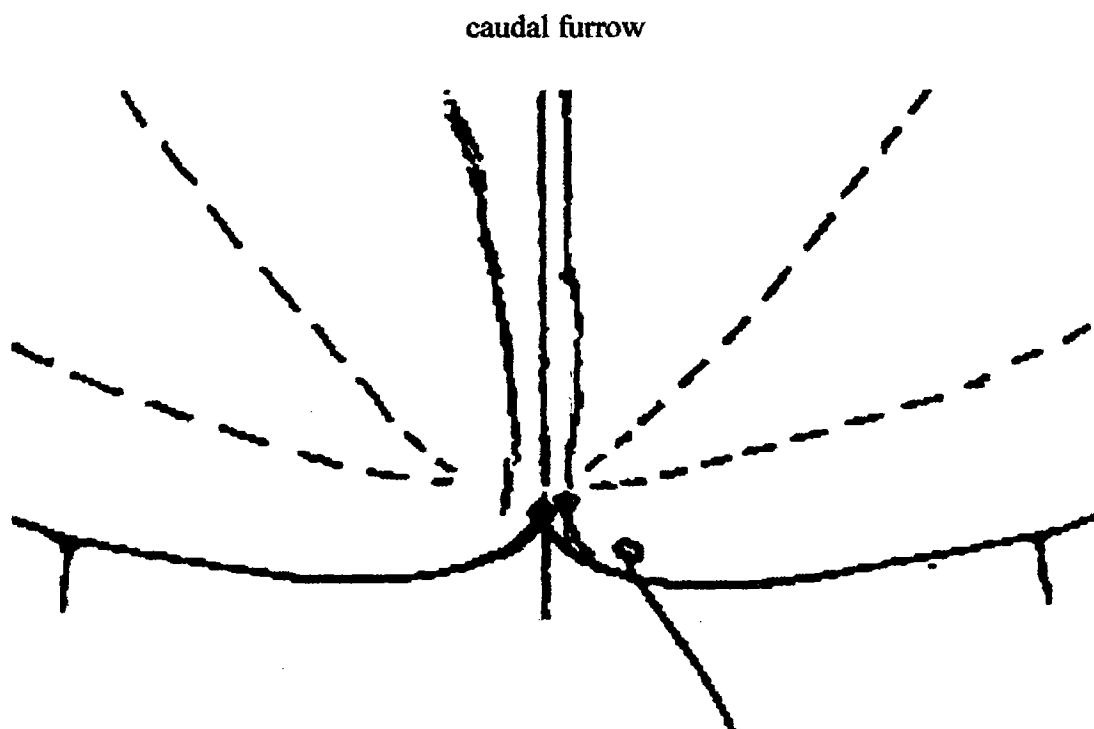


Fig. 6. Characters selected for morphometric studies in puparia - caudal furrow

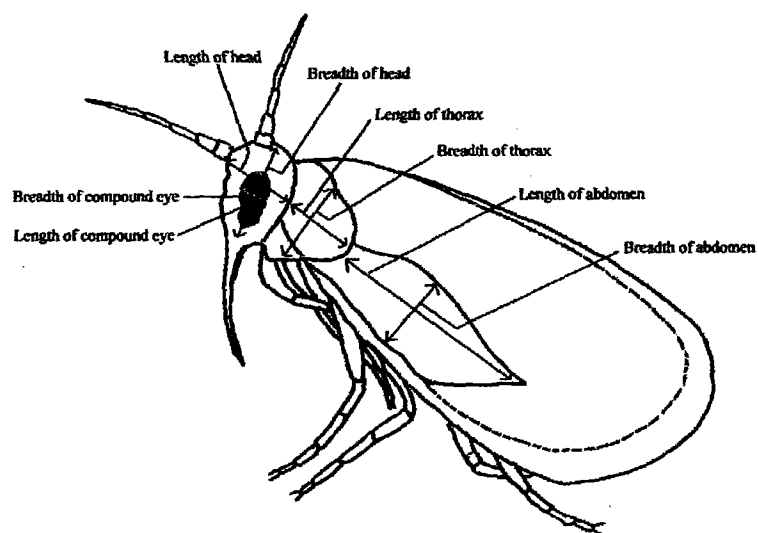


Fig. 7. Characters selected for morphometric studies in adults

Fig. 8. Plot of principal components (Prin2 vs Prin1) of puparia

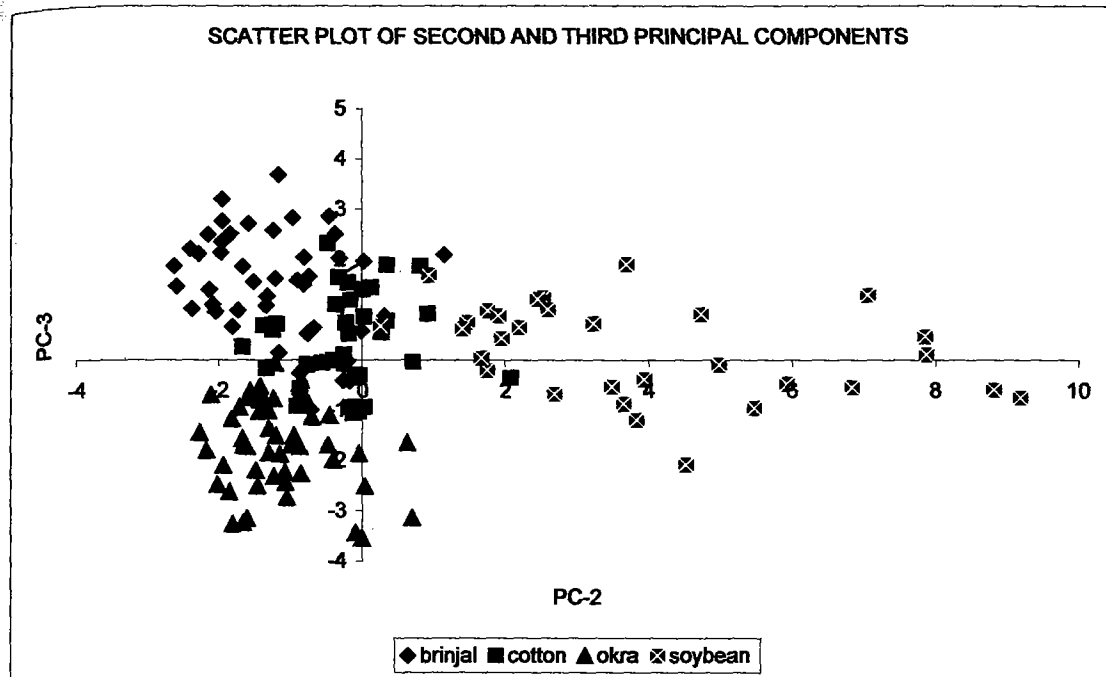


Fig. 9. Plot of principal components (Prin1 vs Prin5) of puparia

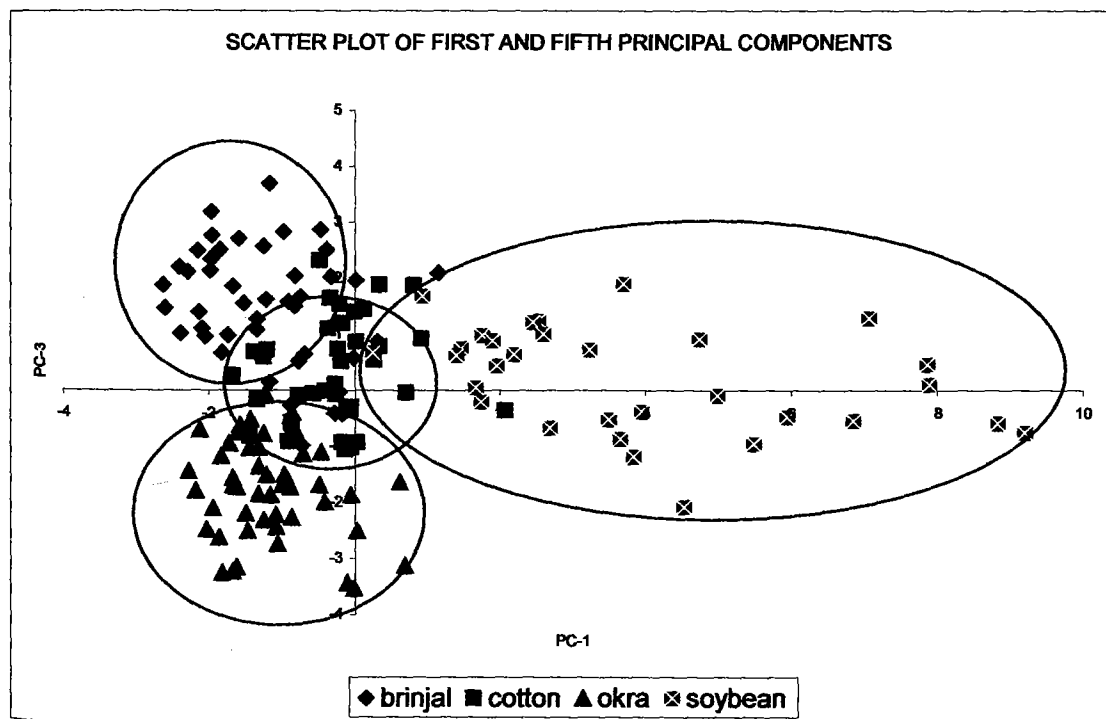


Fig. 10. Plot of principal components (Prin1 vs Prin4) of puparia

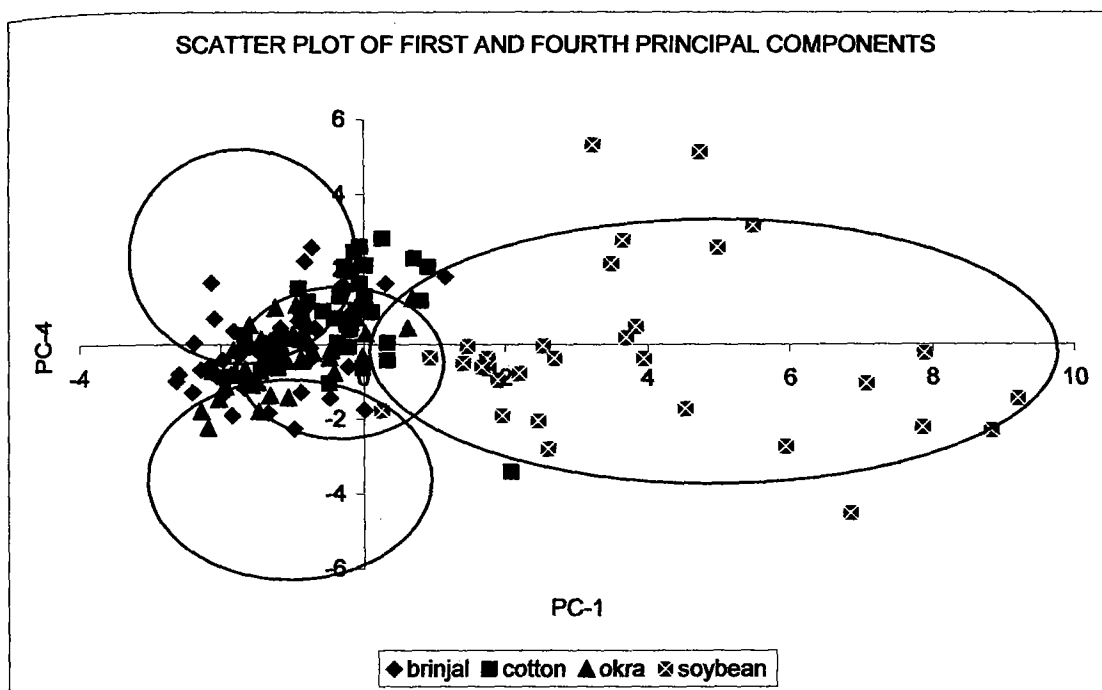


Fig. 11. Plot of principal components (Prin1 vs Prin5) of puparia

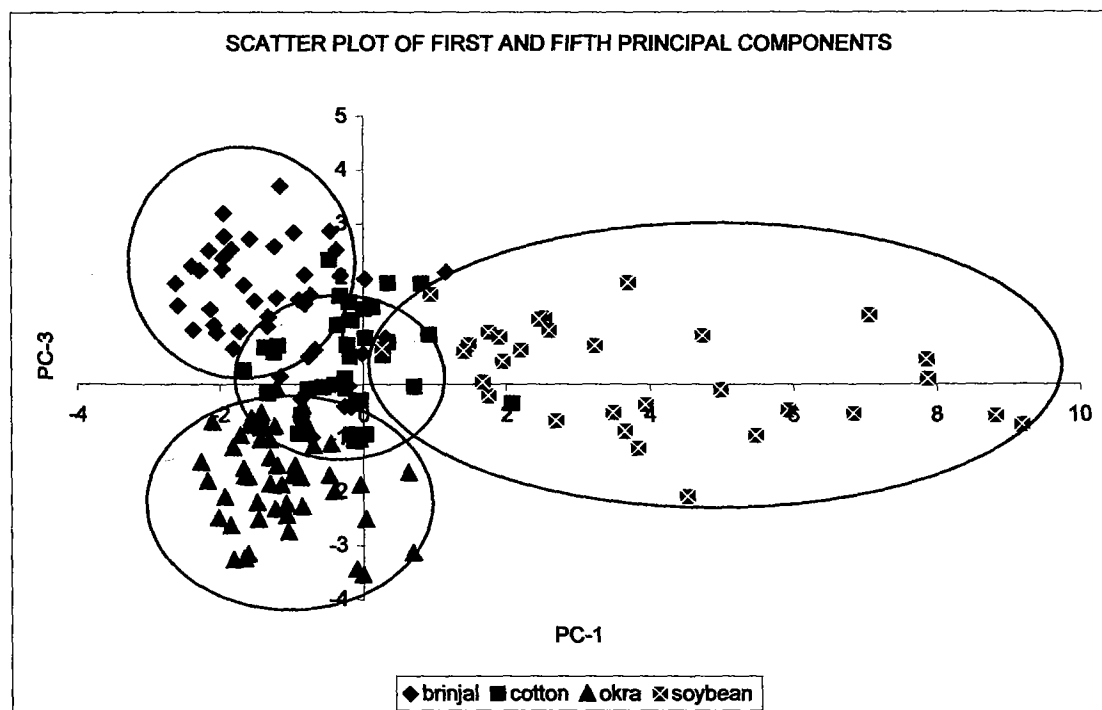


Fig. 12. Plot of principal components (Prin2 vs Prin3) of puparia

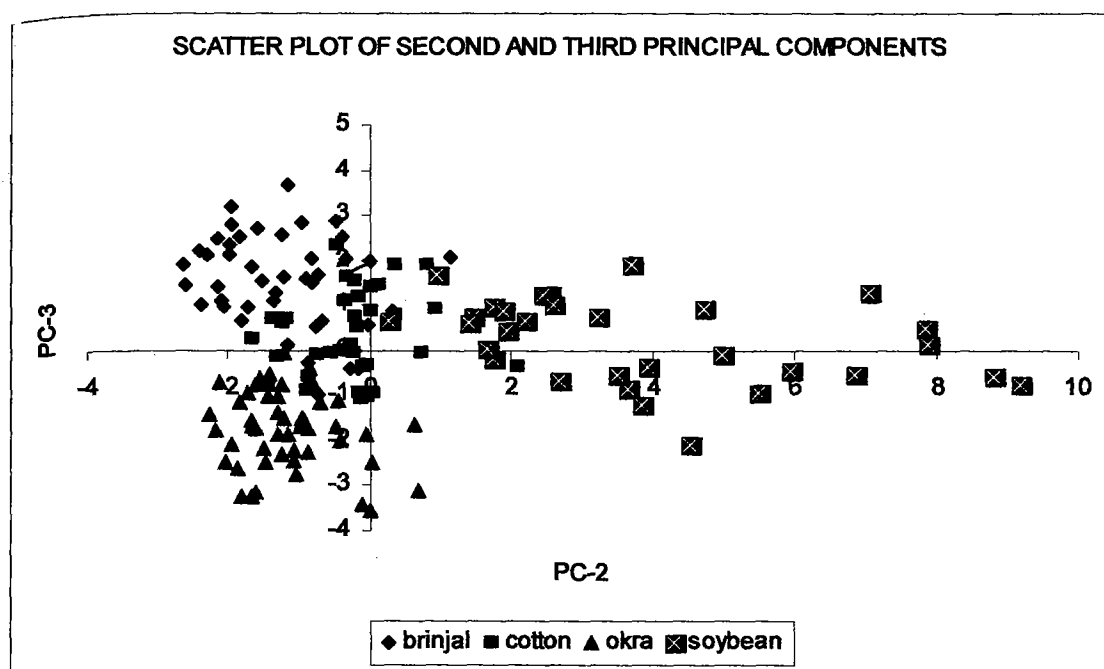


Fig. 13. Plot of principal components (Prin2 vs Prin4) of puparia

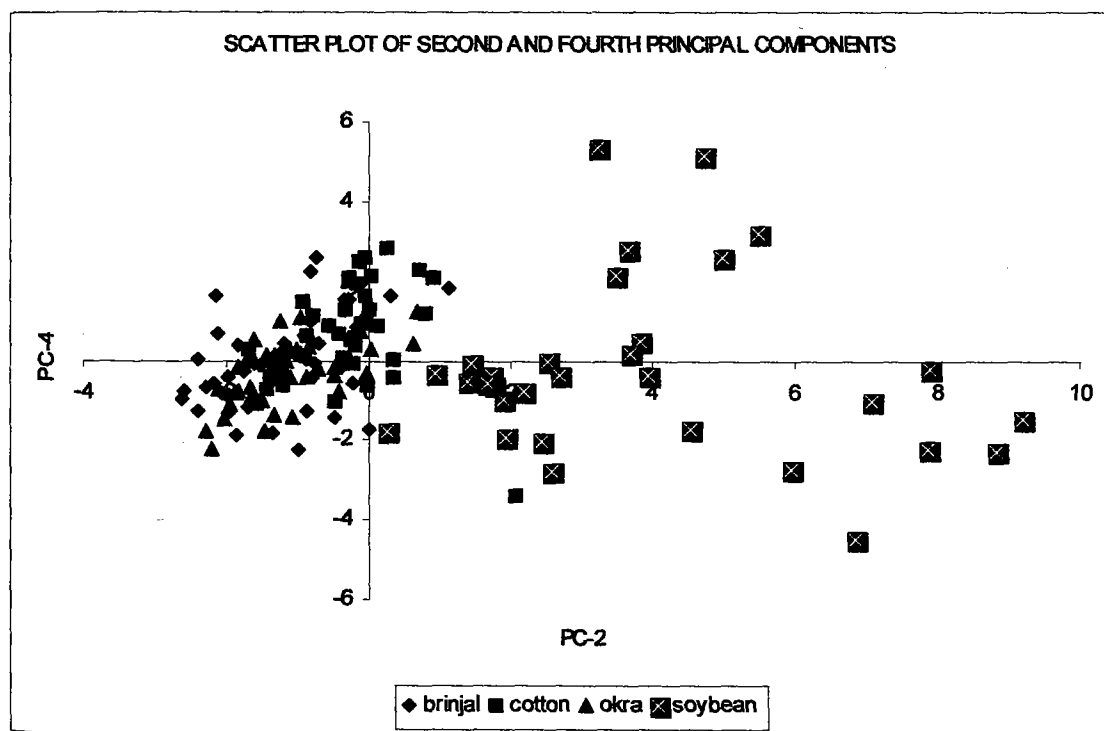


Fig. 14. Plot of principal components (Prin2 vs Prin5) of puparia

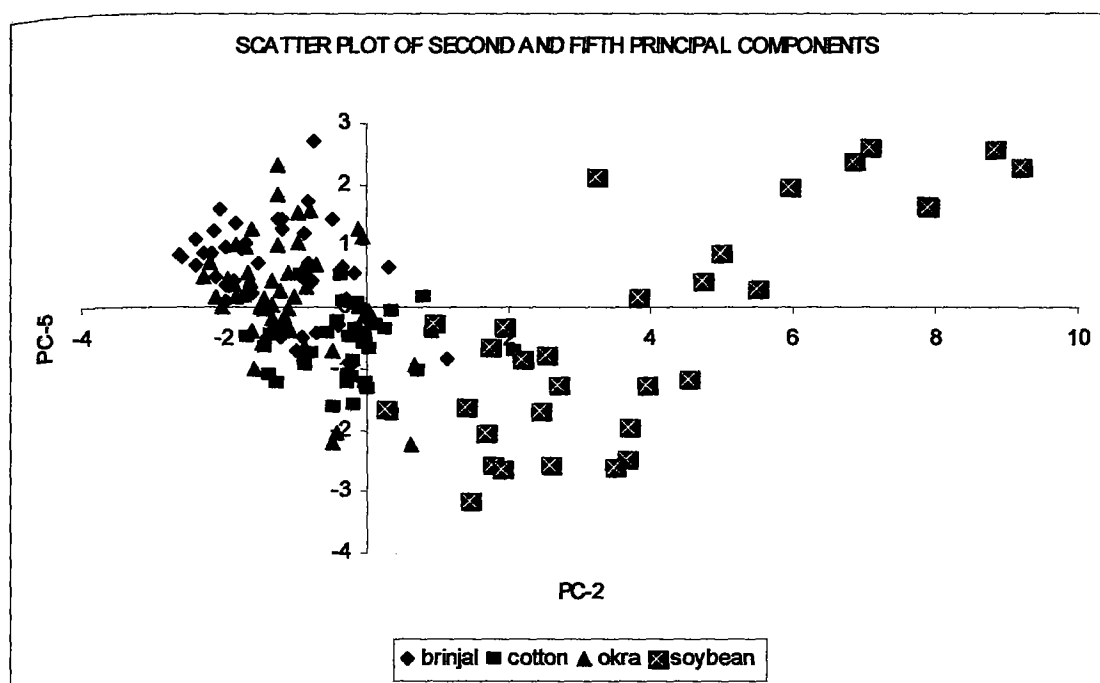


Fig. 15. Plot of principal components (Prin3 vs Prin4) of puparia

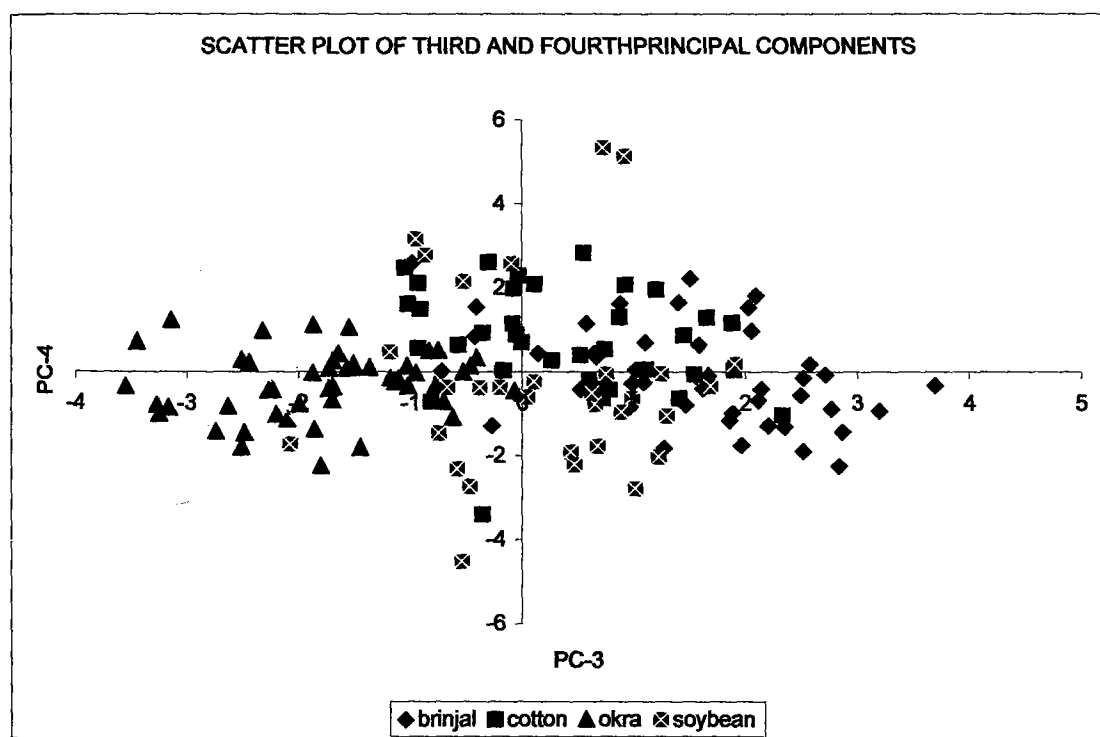


Fig. 16. Plot of principal components (Prin3 vs Prin5) of puparia

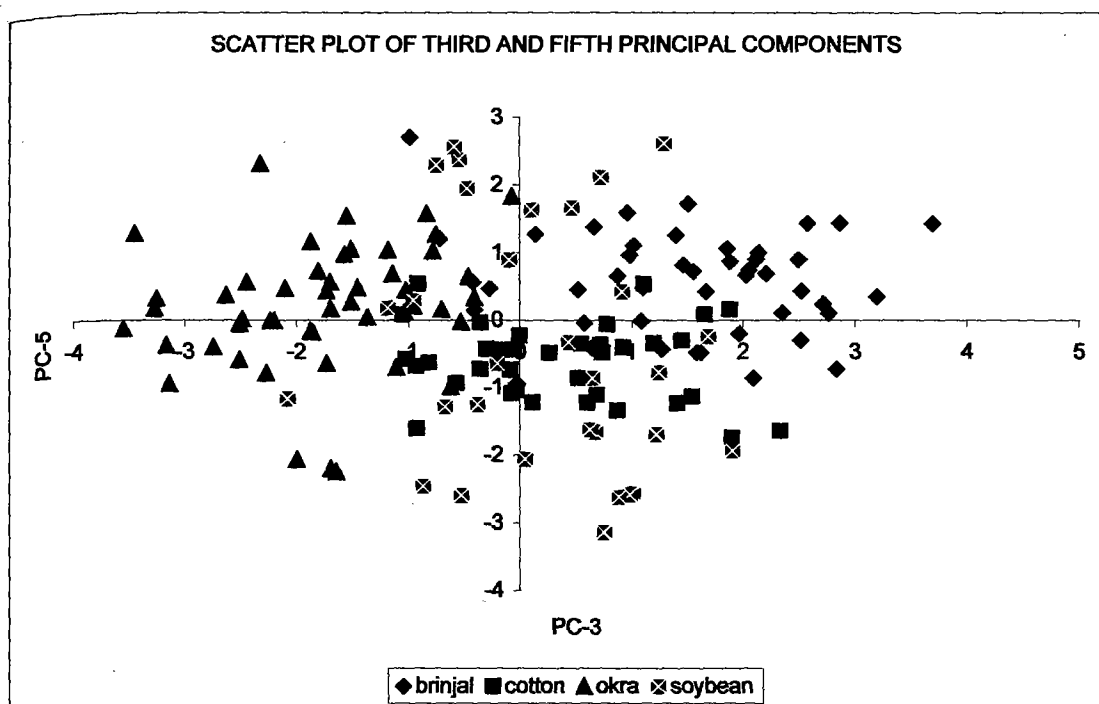


Fig. 17. Plot of principal components (Prin4 vs Prin5) of puparia

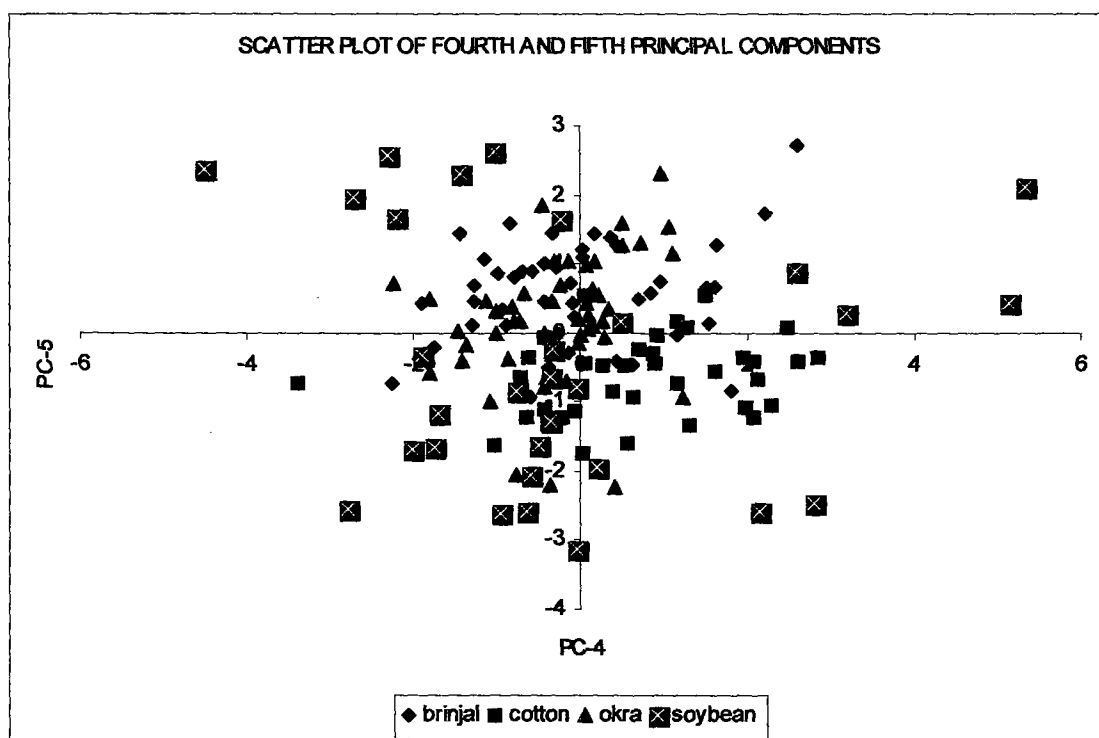


Fig. 18. Plot of principal components (Prin1 and Prin2) of adults

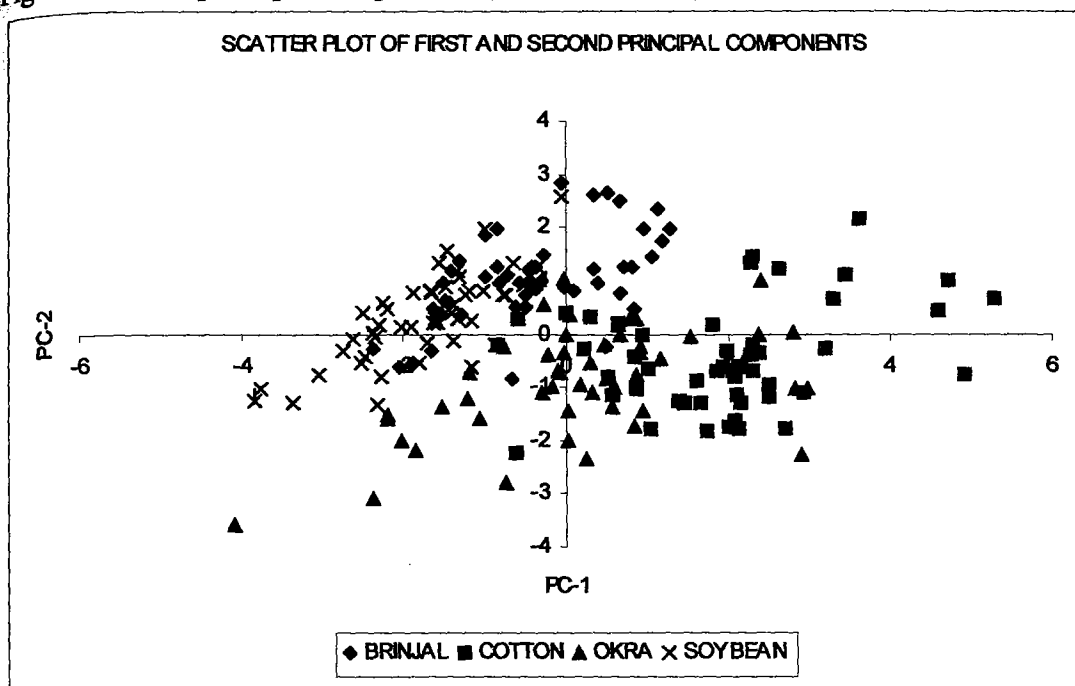


Fig. 19. Plot of principal components (Prin1 vs Prin3) of adults

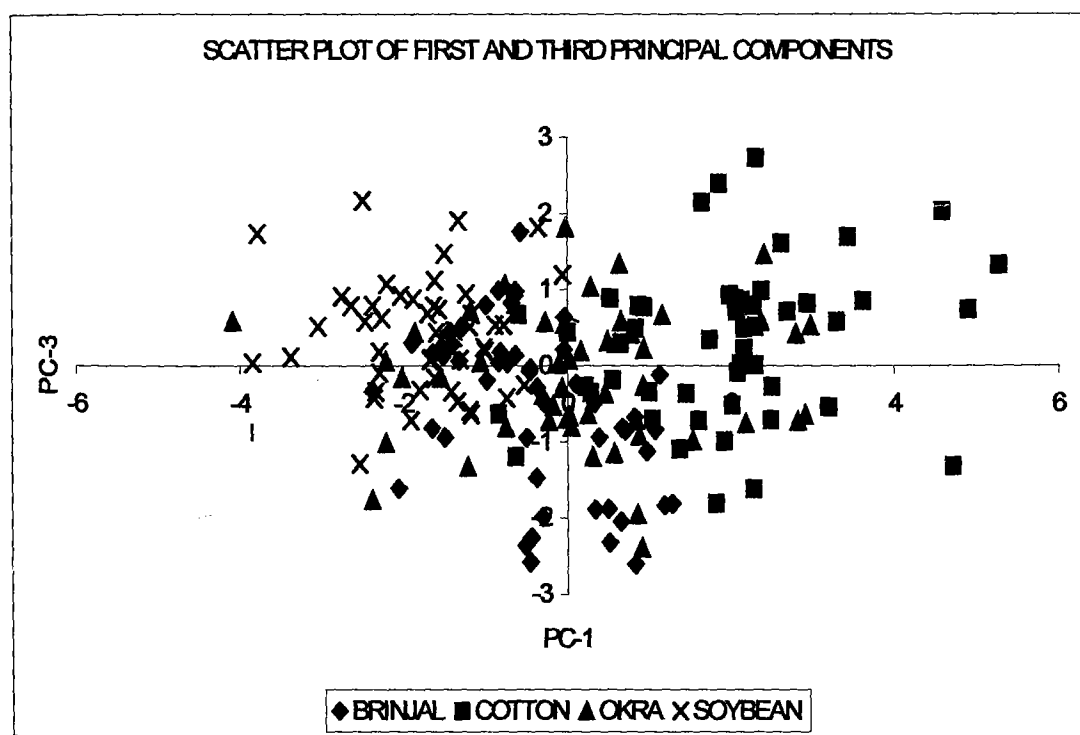


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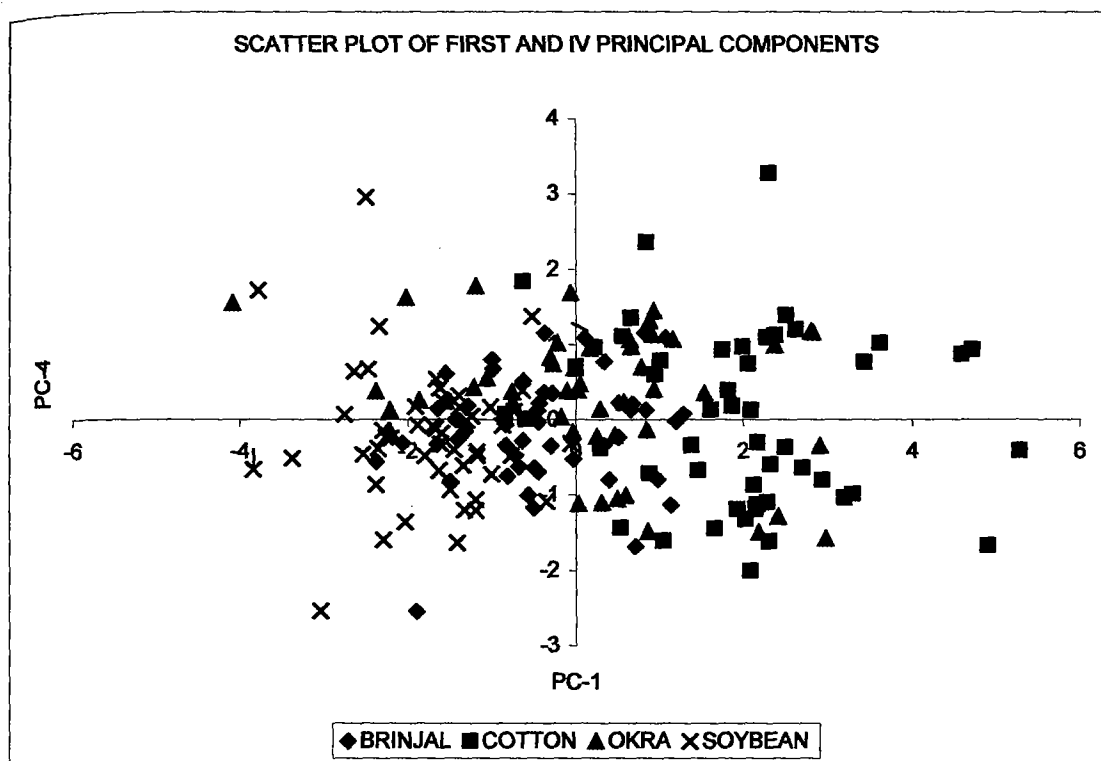


Fig. 21. Plot of principal components (Prin1 vs Prin5) of adults

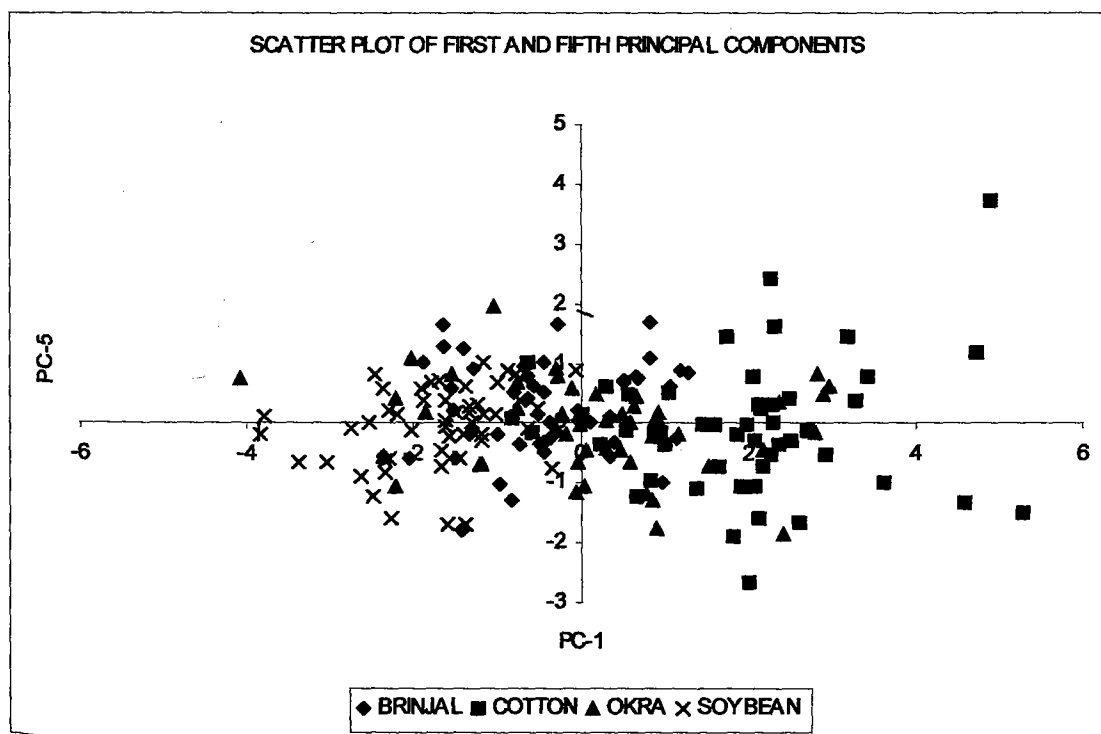


Fig. 22. Plot of principal components (Prin2 vs Prin3) of adults

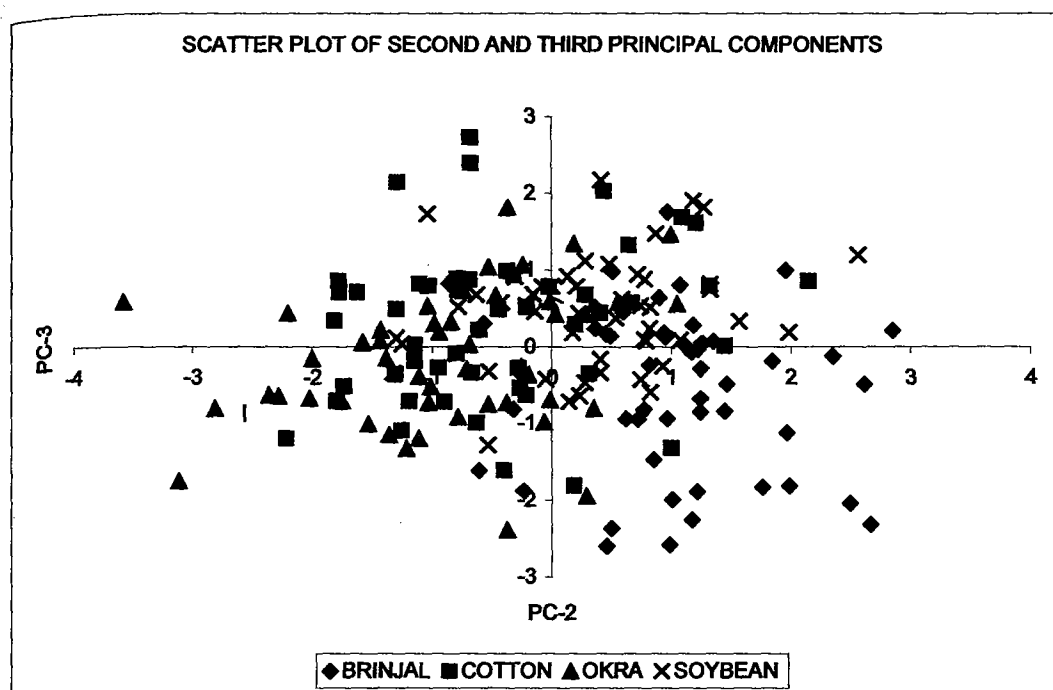


Fig. 23. Plot of principal components (Prin2 vs Prin4) of adults

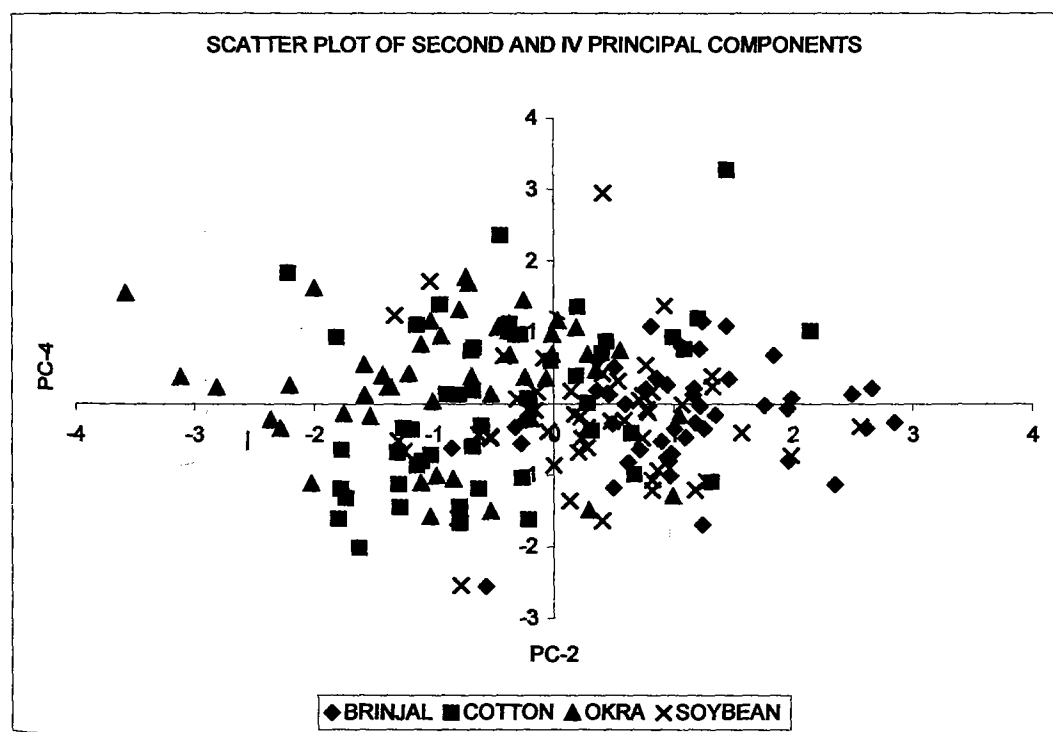


Fig.24. Plot of principal components (Prin2 vs Prin5) of adults

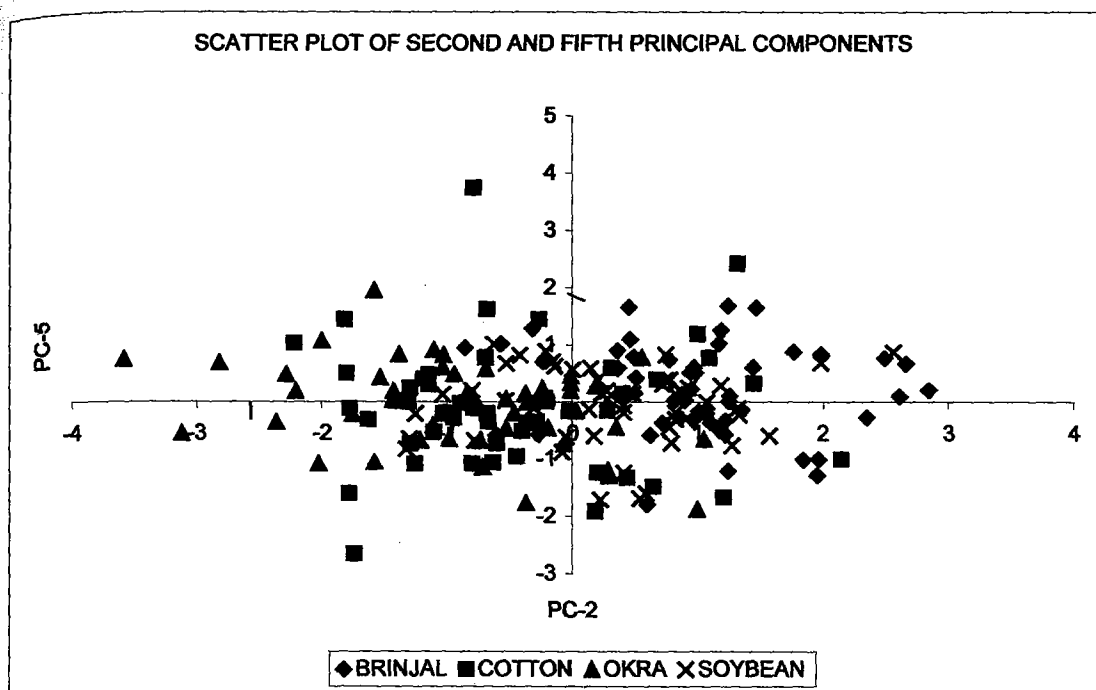


Fig. 25. Plot of principal components (Prin3 vs Prin4) of adults

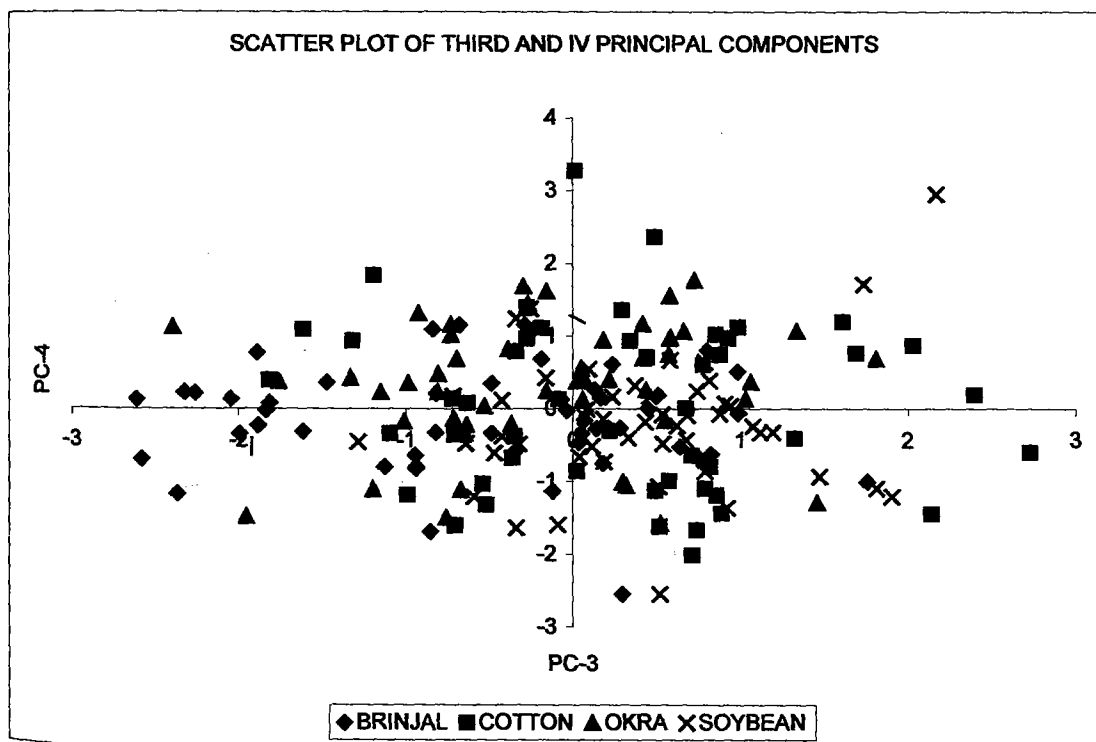


Fig. 26. Plot of principal components (Prin3 vs Prin5) of adults

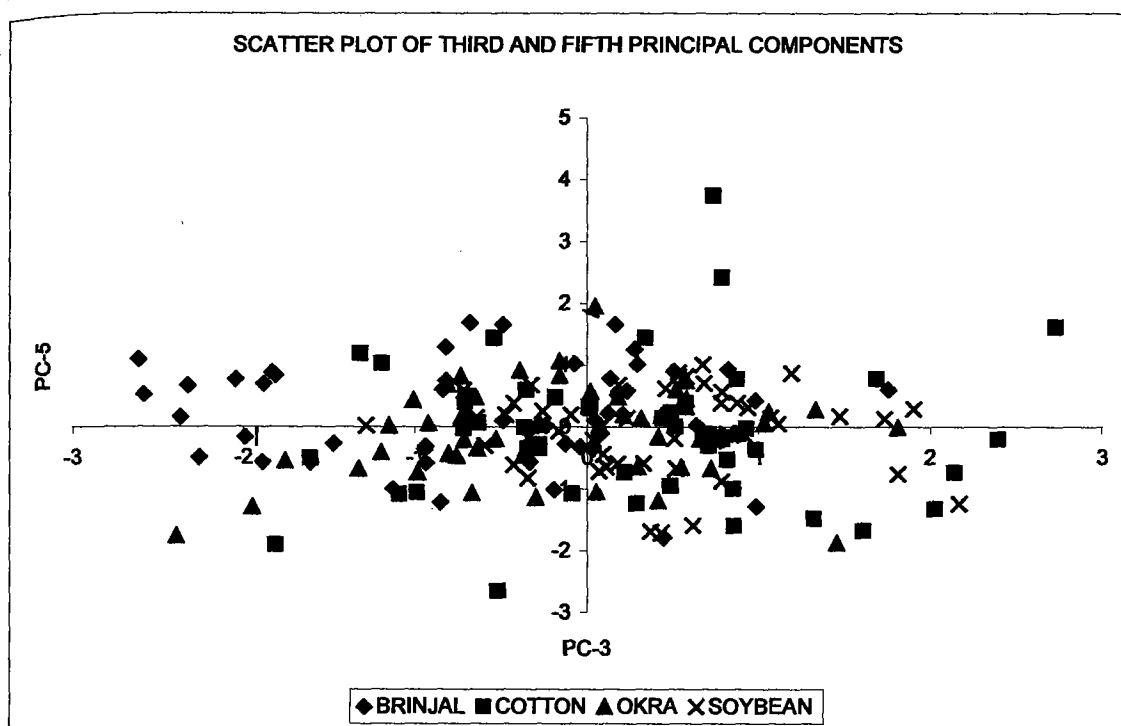
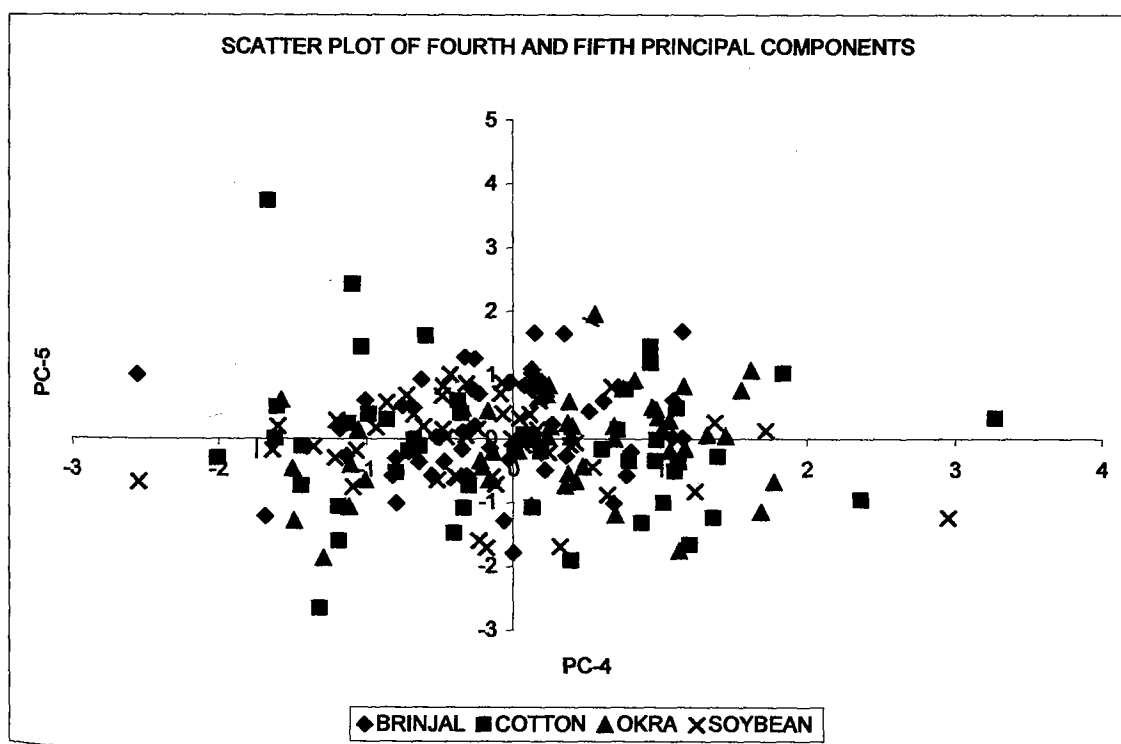


Fig. 27. Plot of principal components (Prin4 vs Prin5) of adults



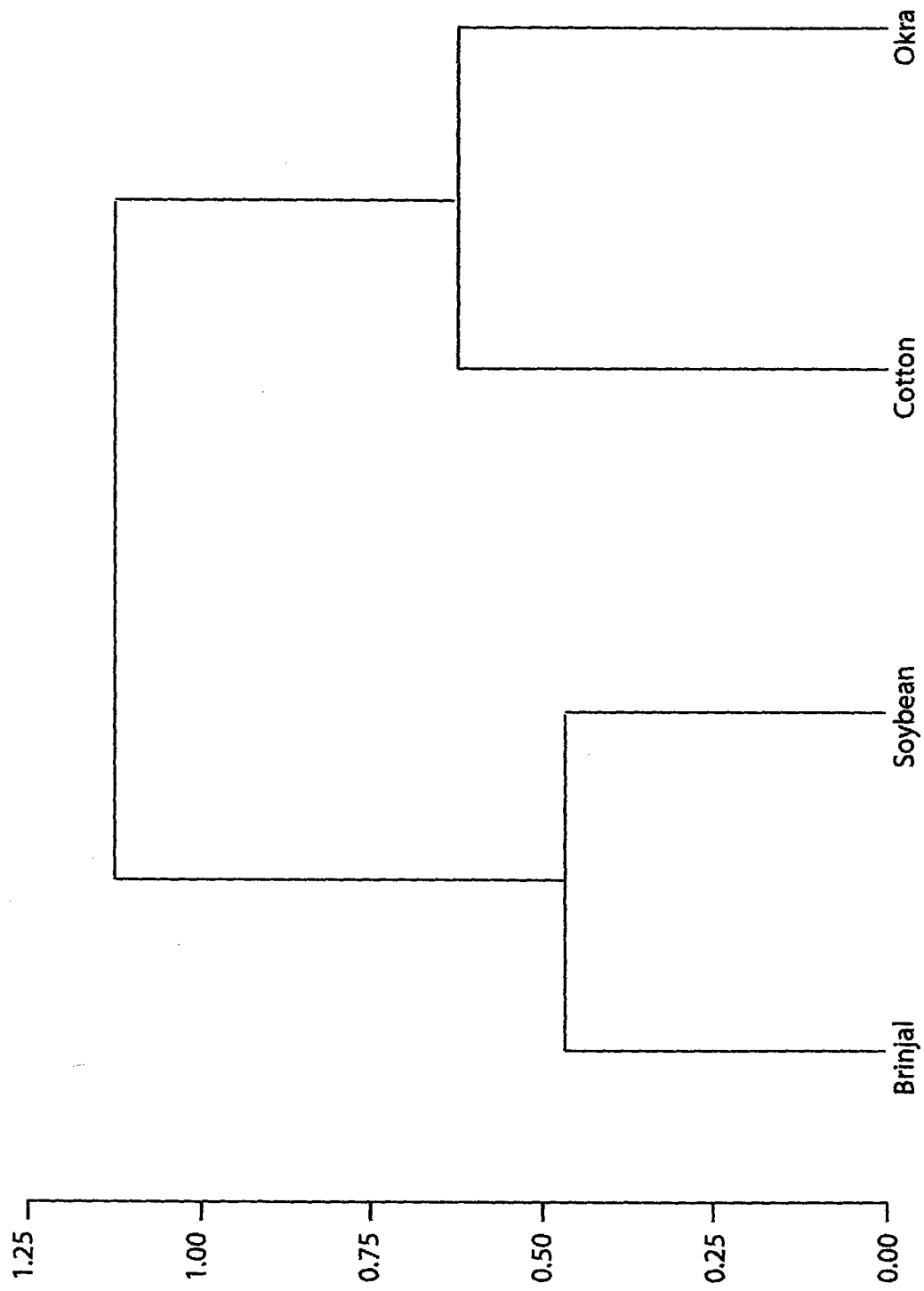


Fig.28 Dendrogram of relationships between four populations obtained through morphometrics of puparia

Figure A. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1-brinjal; Lane2, 3, okra; Lane4,5-soybean; Lane1-5, with B19, A9 and D13 primers, respectively

Figure B. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1, 3-brinjal; Lane4-okra; Lane1 with A11; Lane3-D7; Lane4-B5; Lane2 no sample

Figure C. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1,4 brinjal, Lane 2,3 soybean and okra; Lane1-D18; Lane2-D8; Lane3-D19; Lane4-D16 primers

Figure D. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1-okra population with D6 primers

Figure E. Gel electrophoresis of PCR products with the C4 and C5 primers. Lane M molecular marker 1kb ladder; Lane1-okra with C4 primer and Lane2-soybean with C5 primer

Figure F. Gel electrophoresis of PCR products of cotton (Lane1 with D3 primer). Lane M molecular marker 1kb ladder

Figure G. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1-soybean population with B8 primer; Lane2-okra population with A12 primer

Figure H. Gel electrophoresis of PCR products of cotton with B4 primer. Lane M molecular marker 1kb ladder

Figure I. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1-okra with E8; Lane3-brinjal with D10 primer

Figure J. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane1-soybean population with E20; Lane2, 3, 4 brinjal whitefly population with A10, A14 and A16; Lane6, 9-cotton population with B3, C19; Lane10, 11, 12 okra whitefly population with E13, C18, and C10 primers. Lane 13-cotton with B9.

Figure K. Gel electrophoresis of PCR products of brinjal population primer with E9 primer. Lane M molecular marker 1kb ladder; Lane1-brinjal, amplicon of E9 primer

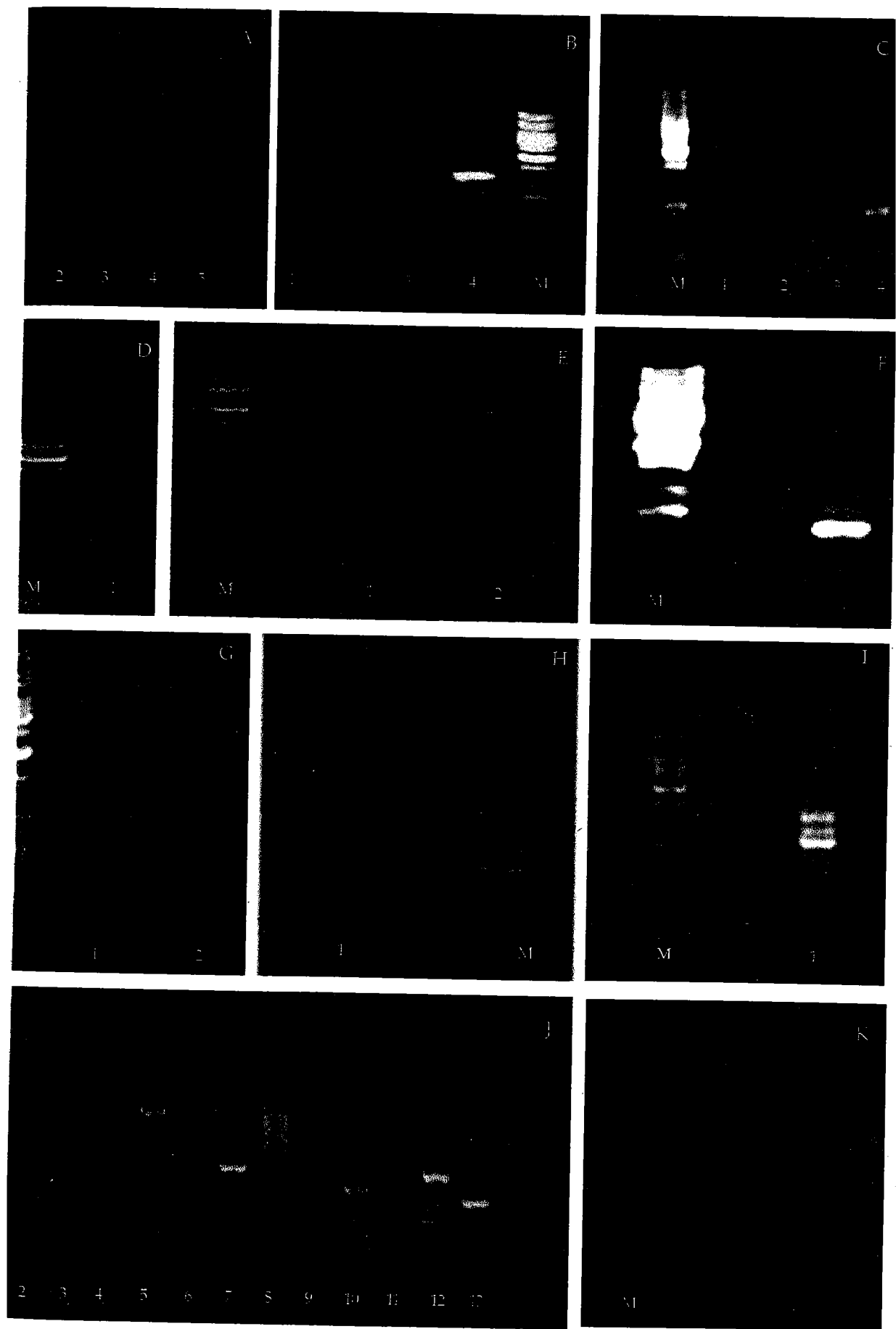


Fig. 29

Figure L. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane 2-okra whitefly population with E5 primer; Lane 4-soybean population with A6 primer and Lane 5-okra population with D5 primer; In Lane 1, 3 samples not loaded

Figure M. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane 1-2 amplicon of D15 primer for okra and brinjal populations

Figure N. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane 1-2 amplicons of B12 primer for brinjal and soybean populations

Figure O. Gel electrophoresis of PCR products. Lane M molecular marker 1kb ladder; Lane 2-3 amplicons of soybean and okra population with E4 primer

Figure P. Gel electrophoresis of PCR products obtained in amplicons in Lane 1, 2 and 3 of cotton, soybean and brinjal populations with A13 primers

Figure Q. RAPD-PCR products obtained with operon F2 primer for Brinjal, cotton, okra and soybean population, respectively. M is 1kb molecular marker

Figure R. RAPD-PCR pattern obtained with operon H16 primer. Lane 1-4 brinjal, cotton, okra and soybean population, respectively. M is 1kb molecular marker

Figure S. RAPD-PCR pattern using primers OPF-12 and OPH-09. Lane-M is the 1 kb molecular size maker; Lane 1-8 are amplicons obtained with DNA from brinjal (1,5) cotton (2,6) okra (3,7) and soybean (4,8) with OPF12 (1-4) and OPH9 (5-8) primers

Figure T. Gel electrophoresis of DNA extracted from cotton population, Lane M is molecular marker of 1kb. Lane 1 DNA extracted from a single whitefly by DNeasy Tissue Kit (Qiagen)

Figure U. Gel electrophoresis of DNA extracted from a group of 5 (Lane 3), 8 (Lane 4) and 10 (Lane 5). M is 1kb molecular marker

Figure V. Gel electrophoresis of genomic DNA of single whitefly eluted with 50 microliter elution buffer (Lane 3). Lane M is molecular marker of 1kb ladder

Figure W. Gel electrophoresis of PCR amplification products of DNA from cotton population following optimized conditions. Upper Lane 2 and Lower Lane 1 for amplicon obtained of E4 and F2 primers, respectively. Lane M is molecular marker of 1kb

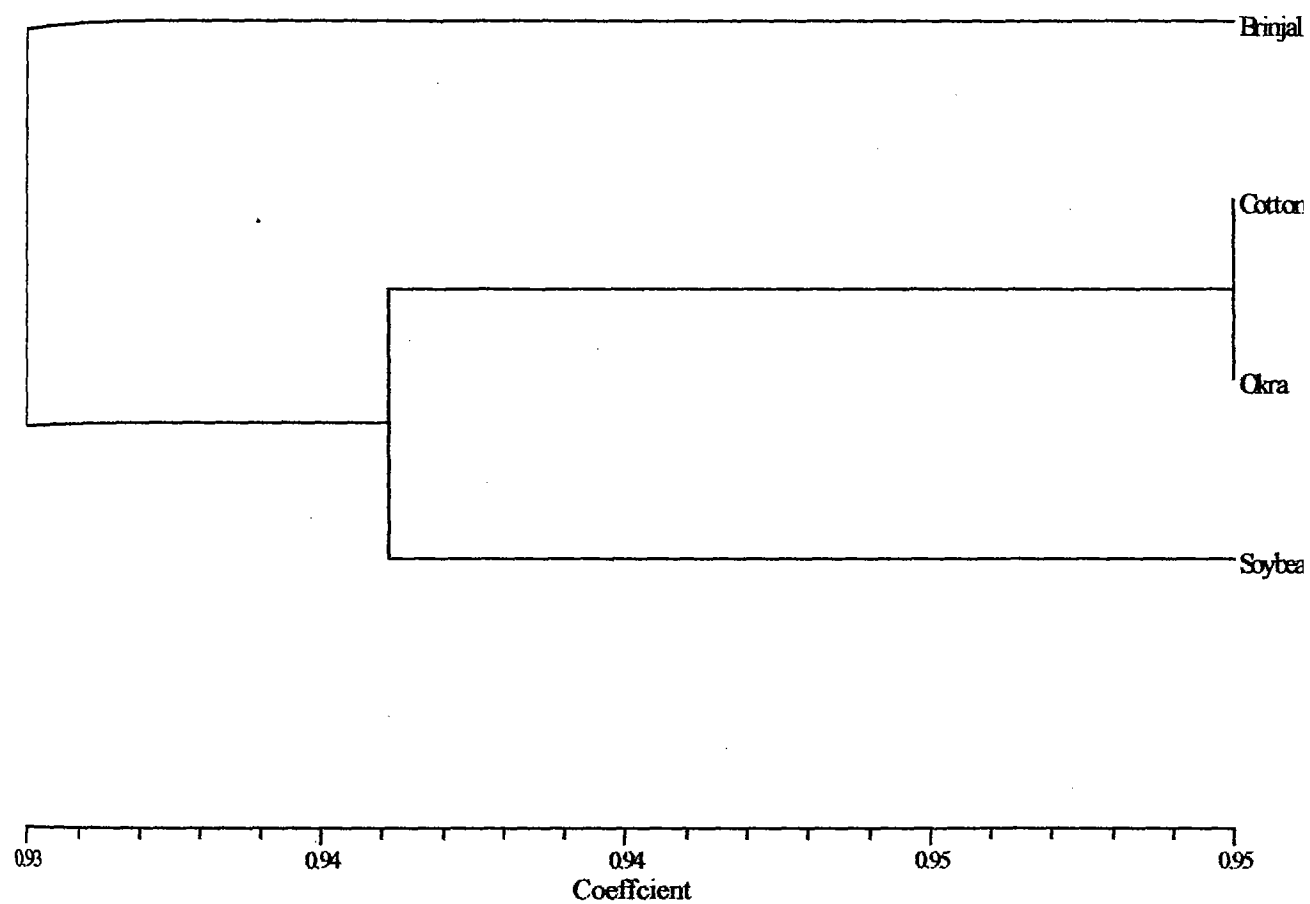


Fig. 30. Dendrogram of relationships between four populations obtained through RAPD-PCR analysis of genomic DNA

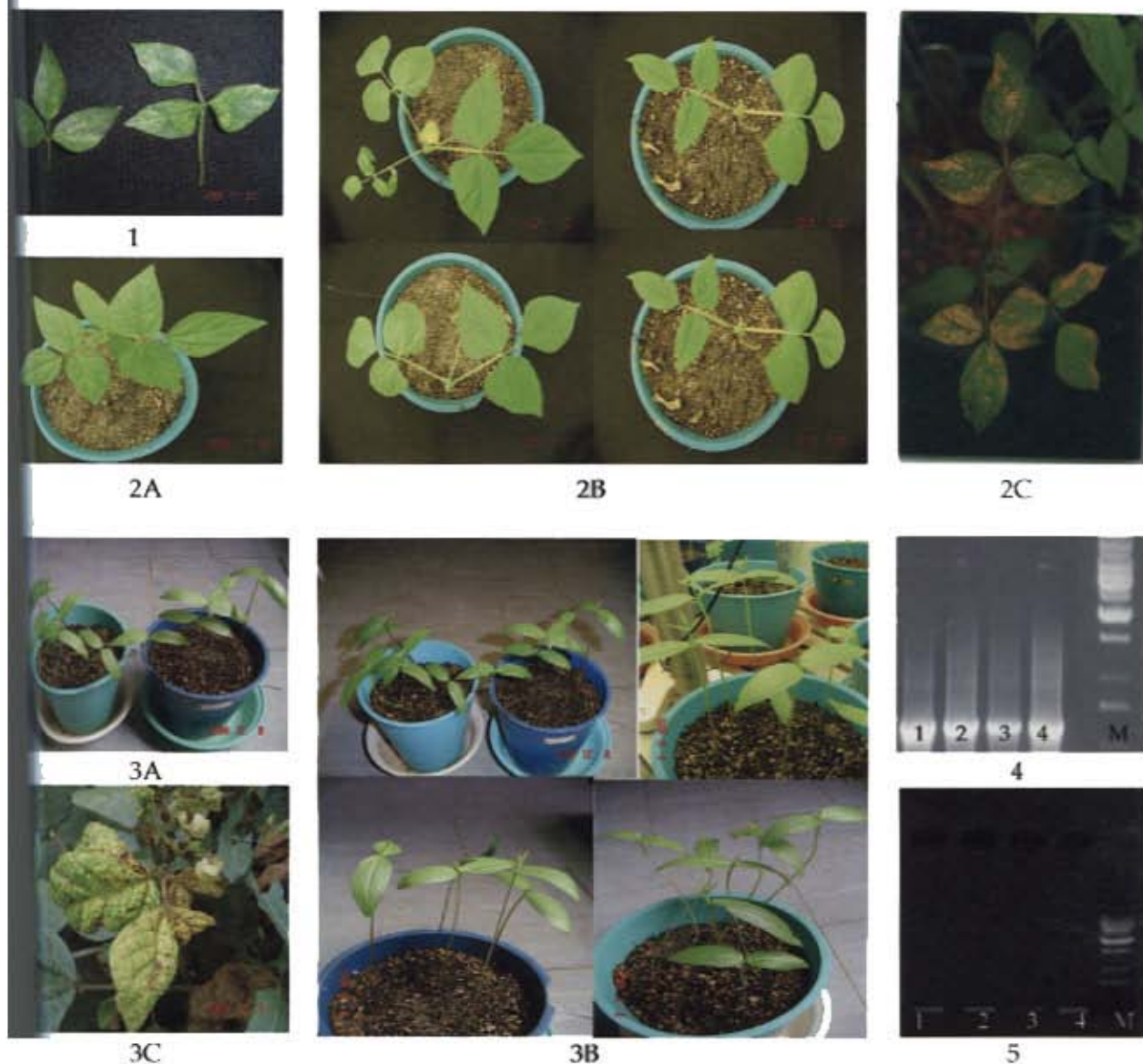


Figure 31-1. Symptoms in MYMIV infected mungbean plant which were used as source

Figure 31-2. Inoculation of soybean seedlings

- A. Healthy uninoculated soybean seedlings
- B. Soybean seedlings with single viruliferous whitefly
- C. Soybean seedlings with fifty viruliferous whiteflies

Figure 31-3. Inoculation of mungbean seedlings

- A. Healthy uninoculated soybean seedlings
- B. Mungbean seedlings with single viruliferous whitefly
- C. Mungbean Soybean seedlings with fifty viruliferous whiteflies

Figure 31-4. PCR detection of MYMIV in soybean inoculated with fifty whiteflies from brinjal (Lane1), cotton (Lane2), okra (Lane3) and soybean (Lane4), respectively

Figure 31-5. PCR detection of MYMIV in the vector from brinjal (Lane1), cotton (Lane2), okra (Lane3) and soybean (Lane4), respectively

Table 1. List of characters considered and selected for morphometric studies of pupa (those with* are characters selected)

S.No.	Character No.	Character
1	1	Length*
2	2	Breadth at apex*
3	3	Breadth at middle*
4	4	Breadth at base*
5	5	Breadth of submargin*
6	-----	Length of transverse moulting suture (TMS)
7	-----	Breadth at right extreme end of TMS
8	-----	Breadth at close to right extreme end of TMS
9	-----	Breadth at left extreme end of TMS
10	-----	Breadth at close to left extreme end of TMS
11	-----	Distance of TMS from anterior mid-point
12	-----	Distance of TMS from posterior mid-point
13	-----	Length of caudal tracheal fold
14	-----	Breadth of tracheal fold at apex
15	-----	Breadth of tracheal fold at middle
16	-----	Breadth of tracheal fold at base
17	6	Length of Abdominal segment 1*
18	8	Length of Abdominal segment 2*
19	10	Length of Abdominal segment 3*
20	12	Length of Abdominal segment 4*
21	14	Length of Abdominal segment 5*
22	16	Length of Abdominal segment 6*
23	18	Length of Abdominal segment 7*
24	20	Length of Abdominal segment 8*
25	7	Breadth of abdominal segment 1*
26	9	Breadth of abdominal segment 2*
27	11	Breadth of abdominal segment 3*
28	13	Breadth of abdominal segment 4*
29	15	Breadth of abdominal segment 5*
30	17	Breadth of abdominal segment 6*
31	19	Breadth of abdominal segment 7*
32	21	Breadth of abdominal segment 8*
33	22	Length of caudal furrow*
34	23	Breadth of caudal furrow at apex*
35	24	Breadth of caudal furrow at middle*
36	25	Breadth of caudal furrow at base*
37	26	Length of operculum*
38	27	Breadth of operculum at apex*
39	28	Breadth of operculum at middle*
40	29	Breadth of operculum at base*
41	30	Length of lingula*
42	31	Breadth of lingula at apex*

43	32	Breadth of lingula at middle*
44	33	Breadth of lingula at base*
45	35	Length of vasiform orifice*
46	36	Breadth of vasiform orifice at apex*
47	37	Breadth of vasiform orifice near apex*
48	38	Breadth of vasiform orifice near base*
49	39	Breadth of vasiform orifice at base*
50	----	Distance of vasiform orifice from anterior mid point
51	----	Length of dorsal seta 1
52	----	Breadth of dorsal seta 1
53	----	Distance of dorsal setae 1 from anterior mid point
54	----	Length of dorsal seta 2
55	----	Breadth of dorsal seta 2
56	----	Distance of dorsal setae 2 from anterior mid point
57	----	Length of dorsal seta 3
58	----	Breadth of dorsal seta 3
59	----	Distance of dorsal setae 3 from anterior mid point
60	----	Length of dorsal seta 4
61	----	Breadth of dorsal seta 4
62	----	Distance of dorsal setae 4 from anterior mid point
63	----	Length of dorsal seta 5
64	----	Breadth of dorsal seta 5
65	----	Distance of dorsal setae 5 from anterior mid point
66	----	Length of dorsal seta 6
67	----	Breadth of dorsal seta 6
68	----	Distance of dorsal setae 6 from anterior mid point
69	----	Length of dorsal seta 7
70	----	Breadth of dorsal seta 7
71	----	Distance of dorsal setae 7 from anterior mid point
72	----	Length of dorsal seta 8
73	----	Breadth of dorsal seta 8
74	----	Distance of dorsal setae 8 from anterior mid point
75	----	Length of right caudal seta
76	34	Breadth of right caudal seta*
77	----	Distance between the caudal setae

Table 2. List of characters considered and selected for morphometric studies of adults
(those with* are characters selected)

S. No.	Character No.	Character
1	----	Length of antennal segment 1
2	----	Length of antennal segment 2
3	----	Length of antennal segment 3
4	----	Length of antennal segment 4
5	----	Length of antennal segment 5
6	----	Length of antennal segment 6
7	----	Length of antennal segment 7
8	----	Breadth of antennal segment 1
9	----	Breadth of antennal segment 2
10	----	Breadth of antennal segment 3
11	----	Breadth of antennal segment 4
12	----	Breadth of antennal segment 5
13	----	Breadth of antennal segment 6
14	----	Breadth of antennal segment 7
15	15	Length of proboscis*
16	16	Breadth of proboscis*
17	17	Length of head*
18	18	Breadth of head*
19	19	Length of compound eye*
20	20	Breadth of compound eye*
21	21	Length of thorax*
22	22	Breadth of thorax*
23	23	Length of abdomen*
24	24	Breadth of abdomen*

Table 3. Details of sequences of the primers used in the study

Code	5'	to	3'	Code	5'	to	3'	Code	5'	to	3'	Code	5'	to	3'
KIT A															
OPA-01	CAGGCCCTTC			OPA-06	GGTCCCTGAC			OPA-11	CAATGGCCGT			OPA-16	AGCCAGCGAA		
OPA-02	TGCCGAGCTG			OPA-07	GAAACGGGTG			OPA-12	TCGGCGATAG			OPA-17	GACCGCTTGT		
OPA-03	ATGCAGCCAC			OPA-08	GTGACGTAGG			OPA-13	CAGCACCCAC			OPA-18	AGGTGACCGT		
OPA-04	AATCGGGCTG			OPA-09	GGGTAACGCC			OPA-14	TCTGTGCTGG			OPA-19	CAAACGTCGG		
OPA-05	AGGGGTCTTG			OPA-10	GTGATCGCAG			OPA-15	TTCCGAACCC			OPA-20	GTTGCGATCC		
KIT B															
OPB-01	GTTTCGDTC			OPB-06	TGCTCTGCCC			OPB-11	GTAGACCCGT			OPB-16	TTTGCCCGGA		
OPB-02	TGATCCCTGG			OPB-07	GGTGACGCAG			OPB-12	CCTTGACGCA			OPB-17	AGGGAACGAG		
OPB-03	CGATCCCTGG			OPB-08	CGCCACACGG			OPB-13	TTCCCCCGCT			OPB-18	CCACAGCAGT		
OPB-04	GGACTGGAGT			OPB-09	TGGGGGACTC			OPB-14	TCCGCTCTGG			OPB-19	ACCCCCGAAG		
OPB-05	TGCGCCCTTC			OPB-10	CTGCTGGGAC			OPB-15	GGAGGGTGTT			OPB-20	GGACCCTTAC		
KIT C															
OPC-01	TTCGAGCCAG			OPC-06	GAACGGACTC			OPC-11	AAAGCTGCGG			OPC-16	CACACTCCAG		
OPC-02	GTGAGGCGTC			OPC-07	GTCCCGACGA			OPC-12	TGTCATCCCC			OPC-17	TTCCCCCAG		
OPC-03	GGGGGTCTTT			OPC-08	TGGACCGGTG			OPC-13	AAGCCTCGTC			OPC-18	TGAGTGGGTG		
OPC-04	COGCATCTAC			OPC-09	CTCACCGTCC			OPC-14	TGCGCTCTTG			OPC-19	GTTGCCAGCC		
OPC-05	GATGACCGCC			OPC-10	TGTCTGGGTG			OPC-15	GACGGATCAG			OPC-20	ACTTCGCCAC		
KIT D															
OPD-01	ACCGCGAAGG			OPD-06	ACCTGAACGG			OPD-11	AGCGCCATTG			OPD-16	AGGGCGTAAG		
OPD-02	GGACCCAACC			OPD-07	TTGGCACGGG			OPD-12	CACCGTATCC			OPD-17	TTTCCCACGG		
OPD-03	GTCGCCGTCA			OPD-08	GTGTGCCCCA			OPD-13	GGGGTGACGA			OPD-18	GAGAGCCAAC		
OPD-04	TCTGGTGAGG			OPD-09	CTCTGGAGAC			OPD-14	CTTCCCCAAG			OPD-19	CTGGGGACTT		
OPD-05	TGAGCGGACA			OPD-10	GGTCTACACC			OPD-15	CATCCGTGCT			OPD-20	ACCCGGTAC		
KIT E															
OPE-01	CCCAAGGTCC			OPE-06	AAGACCCCTC			OPE-11	GAGTCTCAGG			OPE-16	GGTGACTGTG		
OPE-02	GGTGCGGGAA			OPE-07	AGATGCAGCC			OPE-12	TTATCGCCCC			OPE-17	GGTGACTGTG		
OPE-03	CCAGATGCAC			OPE-08	TCACCACGGT			OPE-13	CCCATTCCGG			OPE-18	GGACTGCAGA		
OPE-04	GTGACATGCC			OPE-09	CTTCACCCGA			OPE-14	TGCGGCTGAG			OPE-19	ACGGCGTATG		
OPE-05	TCAGGGAGGT			OPE-10	CACCAGGTGA			OPE-15	ACGCACAACC			OPE-20	AACGGTGACC		
OPF-02 GAGGATCCCT															
OPF-12 ACGGTACCAG															
OPH-09 TGTAGCTGGG															
OPH-16 TCTCAGCTGG															

Table 4. Statistically significant and non-significant characters of puparia (in descending order of their F values)

A. Significant:

Character No.	Group No.	Characters	P Value	F Value
5	G14	Breadth of submargin	3.57×10^{-85}	481.95
34	G14	Breadth of caudal seta	9.26×10^{-67}	335.06
24	G14	Breadth of caudal furrow at middle	2.04×10^{-32}	81.34
23	G14	Breadth of caudal furrow at apex	7.5×10^{-28}	65.01
25	G14	Breadth of caudal furrow at base	3.15×10^{-26}	59.98
21	G14	Breadth of abdominal segment 8	9.3×10^{-22}	46.57
27	G14	Breadth of operculum at apex	5.62×10^{-16}	31.45
38	G14	Breadth of vasiform orifice near base	1.24×10^{-14}	28.22
11	G14	Breadth of abdominal segment 3	6.36×10^{-14}	26.16
30	G14	Length of lingula	3.24×10^{-13}	24.96
22	G14	Length of caudal furrow	1.64×10^{-12}	23.18
3	G14	Breadth at middle	2.84×10^{-12}	22.23
26	G14	Length of operculum	4.79×10^{-12}	22.12
7	G14	Breadth of abdominal segment 1	2.14×10^{-11}	20.58
36	G21	Breadth of vasiform orifice at apex	1.41×10^{-10}	19.09
4	G21	Breadth at base	2.32×10^{-10}	18.23
32	G21	Breadth of lingula at middle	6.22×10^{-10}	17.72
29	G21	Breadth of operculum at base	6.26×10^{-10}	17.68
9	G21	Breadth of abdominal segment 2	7.29×10^{-10}	17.37
2	G21	Breadth of puparia at apex	1.26×10^{-9}	18.38
8	G21	Length of abdominal segment 2	1.68×10^{-9}	16.63
6	G21	Length of abdominal segment 1	3.01×10^{-9}	16.13
1	G21	Length of puparia	4.26×10^{-9}	15.70
10	G21	Length of abdominal segment 3	5.15×10^{-9}	15.66
14	G21	Length of abdominal segment 5	3.02×10^{-8}	14.11
28	G21	Breadth of operculum at middle	8.42×10^{-8}	13.26
37	G21	Breadth of vasiform orifice near apex	1.94×10^{-7}	12.72
12	G21	Length of abdominal segment 4	1.74×10^{-7}	12.63
16	G21	Length of abdominal segment 6	1.76×10^{-7}	12.62
13	G21	Breadth of abdominal segment 4	2.62×10^{-6}	10.60
18	G21	Length of abdominal segment 7	2.69×10^{-6}	10.60
15	G21	Breadth of abdominal segment 5	2.25×10^{-6}	10.51
39	G21	Breadth of vasiform orifice at base	8.9×10^{-6}	9.44
20	G21	Length of abdominal segment 8	1.62×10^{-5}	8.94
31	G21	Breadth of lingula at base	6.0×10^{-4}	6.06
17	G2	Breadth of abdominal segment 6	0.02	3.38
35	G2	Length of vasiform orifice	0.05	2.72

B. Non-significant:

Character No.	Group No.	Characters	P Value	F Value
33	NS	Breadth of lingula at base	0.07	2.36
19	NS	Breadth of abdominal segment 7	0.32	1.19

Table 5. List of statistically significant characters of puparia (based on their location in the body)

Character No.	Group No.	Characters	P Value	F Value
		Puparia		
1	G21	Length	4.26×10^{-9}	15.70
2	G21	Breadth at apex	1.26×10^{-9}	18.38
3	G14	Breadth at middle	2.84×10^{-12}	22.23
4	G21	Breadth at base	2.32×10^{-10}	18.23
5	G14	Breadth of submargin	3.57×10^{-85}	481.95
		Abdominal Segment		
6	G21	Length of abdominal segment 1	3.01×10^{-9}	16.13
7	G14	Breadth of abdominal segment 1	2.14×10^{-11}	20.58
8	G21	Length of abdominal segment 2	1.68×10^{-9}	16.63
9	G21	Breadth of abdominal segment 2	7.29×10^{-10}	17.37
10	G21	Length of abdominal segment 3	5.15×10^{-9}	15.66
11	G14	Breadth of abdominal segment 3	6.36×10^{-14}	26.16
12	G21	Length of abdominal segment 4	1.74×10^{-7}	12.63
13	G21	Breadth of abdominal segment 4	2.62×10^{-6}	10.60
14	G21	Length of abdominal segment 5	3.02×10^{-8}	14.11
15	G21	Breadth of abdominal segment 5	2.25×10^{-6}	10.51
16	G21	Length of abdominal segment 6	1.76×10^{-7}	12.62
17	G2	Breadth of abdominal segment 6	0.019	3.38
18	G21	Length of abdominal segment 7	2.69×10^{-6}	10.60
20	G21	Length of abdominal segment 8	1.62×10^{-5}	8.94
21	G14	Breadth of abdominal segment 8	9.3×10^{-22}	46.57
		Vasiform Orifice		
26	G14	Length of operculum	4.79×10^{-12}	22.12
27	G14	Breadth of operculum at apex	5.62×10^{-16}	31.45
28	G21	Breadth of operculum at middle	8.42×10^{-8}	13.36
29	G21	Breadth of operculum at base	6.26×10^{-10}	17.68
30	G14	Length of lingula	3.24×10^{-13}	24.96
31	G21	Breadth of lingula at apex	6.0×10^{-4}	6.06
32	G21	Breadth of lingula at middle	6.22×10^{-10}	17.72
35	G2	Length of vasiform orifice	0.05	2.72
36	G21	Breadth of vasiform orifice at apex	1.41×10^{-10}	19.09
37	G21	Breadth of vasiform orifice near apex	1.94×10^{-7}	12.72
38	G14	Breadth of vasiform orifice near base	1.24×10^{-14}	28.22
39	G21	Breadth of vasiform orifice at base	8.9×10^{-6}	9.44
		Caudal Furrow		
22	G14	Length of caudal furrow	1.64×10^{-12}	23.18
23	G14	Breadth of caudal furrow at apex	7.5×10^{-28}	65.01
24	G14	Breadth of caudal furrow at middle	2.04×10^{-32}	81.34
25	G14	Breadth of caudal furrow at base	3.15×10^{-26}	59.98
		Caudal Seta		
34	G14	Breadth of caudal seta	9.26×10^{-67}	335.06

Table 6. Morphometrics of puparia in the intraspecific populations – length (observations calibrated to 50x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	0	0	0	26	37	38	34	0
2	0	45	36	45	27	40	43	40	41
3	38	45	45	35	28	35	45	36	44
4	0	45	38	48	29	41	49	35	44
5	41	43	49	40	30	39	45	44	43
6	39	43	27	45	31	42	42	31	38
7	44	46	36	44	32	42	38	47	36
8	38	46	38	40	33	39	46	43	46
9	43	42	37	45	34	41	48	40	41
10	43	47	44	40	35	40	45	41	44
11	45	45	30	45	36	34	42	34	35
12	40	38	32	42	37	40	47	46	42
13	36	41	37	0	38	31	48	35	35
14	39	41	43	35	39	32	38	43	36
15	39	46	42	44	40	32	37	46	47
16	39	46	42	36	41	31	49	44	36
17	36	47	45	40	42	30	0	42	38
18	40	47	47	38	43	32	0	44	44
19	44	48	46	42	44	34	0	48	40
20	34	45	45	40	45	31	0	43	37
21	41	48	37	43	46	34	0	37	40
22	42	38	32	44	47	30	0	38	46
23	40	47	44	40	48	29	0	37	44
24	42	42	42	0	49	34	0	42	37
25	45	40	40	0	50	35	0	44	37

Summary : Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	872.37	290.79	15.70	4.26 x 10 ⁻⁹	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.84	7.88	12.87	9.09	10.61

Crop	n	Mean	SD
Brinjal	47	37.72	4.47
Cotton	40	44.03	3.47
Okra	49	40.16	5.17
Soybean	45	40.93	3.72

Table 7. Morphometrics of puparia in the intraspecific populations – breadth at apex (observations calibrated to 50x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	16	17	21	26	20	19	17	15
2	19	20	19	15	27	15	20	17	13
3	0	20	16	18	28	20	20	16	15
4	20	18	19	15	29	19	19	18	15
5	20	18	12	17	30	20	18	16	15
6	19	18	17	19	31	20	17	18	14
7	17	18	17	18	32	20	20	18	15
8	16	19	16	18	33	20	20	18	15
9	20	19	19	10	34	20	20	16	14
10	20	18	14	12	35	15	18	13	15
11	15	18	15	15	36	20	20	18	18
12	13	18	15	0	37	15	20	16	14
13	20	19	18	12	38	15	18	19	15
14	15	19	16	17	39	15	18	19	11
15	20	20	18	12	40	14	20	18	15
16	20	19	18	15	41	13	0	18	18
17	17	18	18	12	42	15	0	18	18
18	20	18	19	15	43	18	0	18	18
19	15	19	17	15	44	18	0	18	18
20	19	19	16	16	45	16	0	15	18
21	20	19	15	15	46	15	0	15	18
22	20	18	19	15	47	15	0	15	18
23	17	18	17	0	48	19	0	17	18
24	20	18	20	0	49	15	0	16	18
25	16	18	11	0	50	18	0	0	0

Summary : Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	221.81	73.94	18.38	1.26 x 10 ⁻⁹	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.43	5.27	11.13	15.09	11.67

Crop	n	Mean	SD
Brinjal	48	17.67	2.37
Cotton	40	18.73	0.99
Okra	49	16.84	1.87
Soybean	45	15.62	2.36

Table 8. Morphometrics of puparia in the intraspecific populations – breadth at middle (observations calibrated to 50x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	30	23	32	26	27	32	23	29
2	27	28	32	24	27	26	34	25	29
3	0	30	24	25	28	31	34	24	23
4	30	31	28	23	29	24	33	30	26
5	26	30	19	31	30	30	29	24	24
6	30	37	22	26	31	30	26	27	22
7	25	33	25	27	32	31	34	29	29
8	30	32	24	30	33	33	32	28	25
9	33	33	30	22	34	32	33	27	25
10	31	33	19	24	35	24	35	22	25
11	22	26	19	30	36	30	34	31	29
12	24	28	25	0	37	25	34	25	28
13	26	29	30	22	38	25	28	29	20
14	24	34	27	27	39	25	25	30	17
15	28	34	29	15	40	20	37	33	26
16	32	34	34	25	41	19	0	30	29
17	28	33	34	23	42	24	0	30	29
18	34	35	34	25	43	25	0	32	27
19	24	30	33	22	44	23	0	31	26
20	26	34	24	30	45	24	0	24	26
21	25	27	22	25	46	20	0	25	25
22	27	34	29	26	47	20	0	25	27
23	27	30	26	0	48	25	0	30	25
24	27	29	30	0	49	22	0	31	26
25	24	28	20	0	50	25	0	0	0

Summary : Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	882.89	294.30	22.23	2.8×10^{-12}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	14.01	9.68	15.39	13.35	13.21

Crop	N	Mean	SD
Brinjal	48	26.46	3.71
Cotton	40	31.55	3.05
Okra	49	27.08	4.17
Soybean	45	25.58	3.41

Table 9. Morphometrics of puparia in the intraspecific populations – breadth at base (observations calibrated to 50x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	16	17	20	26	20	19	17	15
2	19	17	19	15	27	15	20	17	13
3	0	20	16	18	28	20	20	16	14
4	20	19	19	15	29	19	19	18	15
5	20	18	12	17	30	20	18	16	15
6	19	20	17	19	31	20	17	18	14
7	17	18	17	18	32	20	20	18	15
8	16	24	16	18	33	20	20	18	15
9	20	19	19	10	34	20	20	16	14
10	20	18	12	11	35	15	18	13	15
11	15	18	12	15	36	20	20	18	14
12	13	17	15	0	37	15	20	16	14
13	18	18	18	12	38	15	18	19	18
14	15	19	16	21	39	15	18	19	11
15	20	20	18	13	40	14	20	18	15
16	20	19	18	15	41	13	0	18	18
17	17	18	18	11	42	15	0	18	18
18	20	18	19	15	43	18	0	18	18
19	15	19	17	15	44	18	0	18	18
20	19	19	16	16	45	16	0	15	18
21	20	19	15	15	46	15	0	15	18
22	20	18	19	14	47	15	0	15	18
23	17	18	17	0	48	19	0	17	18
24	19	18	20	0	49	15	0	16	18
25	16	17	11	0	50	18	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	264.34	88.11	18.23	2.32×10^{-10}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.19	5.80	12.30	18.68	12.88

Crop	n	Mean	SD
Brinjal	48	17.60	2.33
Cotton	40	18.77	1.36
Okra	49	16.73	2.05
Soybean	45	15.38	2.73

Table 10. Morphometrics of puparia in the intraspecific populations – breadth of submargin (observations calibrated to 312.50x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	6	7	4	26	10	6	8	5
2	10	7	7	3	27	10	6	6	5
3	0	6	7	4	28	10	7	6	5
4	10	7	7	3	29	9	7	8	5
5	10	8	8	5	30	11	7	6	5
6	9	6	6	4	31	11	7	7	5
7	9	7	7	3	32	10	7	8	5
8	9	6	6	4	33	9	7	7	5
9	10	7	8	4	34	9	7	7	5
10	10	6	6	4	35	9	7	7	5
11	10	6	7	3	36	10	7	8	5
12	9	7	6	0	37	10	7	7	5
13	11	7	7	4	38	10	7	8	4
14	9	7	7	5	39	10	7	7	4
15	11	6	7	5	40	8	7	8	5
16	10	6	7	4	41	10	0	7	5
17	9	6	7	5	42	11	0	7	5
18	10	6	7	4	43	9	0	8	5
19	9	6	7	5	44	10	0	8	5
20	10	6	6	4	45	9	0	7	5
21	10	6	6	4	46	10	0	7	5
22	10	6	7	5	47	9	0	7	5
23	10	7	7	0	48	8	0	7	5
24	10	6	7	0	49	9	0	8	5
25	9	6	6	0	50	9	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	622.37	207.46	481.95	3.57×10^{-15}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	7.49	8.36	9.42	14.57	9.36

Crop	n	Mean	SD
Brinjal	48	9.67	0.72
Cotton	40	6.58	0.55
Okra	49	7.02	0.66
Soybean	45	4.53	0.66

Table 11. Morphometrics of puparia in the intraspecific populations – length of abdominal segment 1 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	184	156	119	26	190	200	170	93
2	154	160	196	114	27	150	210	160	184
3	0	160	146	172	28	180	202	160	170
4	170	190	166	150	29	140	200	150	150
5	160	170	106	210	30	170	176	150	130
6	150	190	152	180	31	170	160	190	0
7	160	184	156	176	32	180	200	184	180
8	158	190	140	170	33	190	166	180	180
9	190	190	160	106	34	180	192	174	150
10	160	200	128	160	35	130	186	140	0
11	140	156	130	200	36	160	204	198	190
12	140	170	158	200	37	138	208	154	160
13	170	170	170	110	38	0	160	170	90
14	138	210	180	170	39	130	140	180	100
15	180	210	170	150	40	130	200	176	120
16	172	190	194	150	41	110	0	190	0
17	164	200	200	150	42	134	0	192	0
18	180	190	190	150	43	156	0	200	0
19	140	200	186	0	44	130	0	190	0
20	190	200	164	188	45	144	0	164	0
21	160	160	140	156	46	124	0	166	0
22	180	210	170	164	47	100	0	162	0
23	150	170	180	93	48	144	0	186	0
24	140	176	180	0	49	130	0	174	0
25	130	170	120	0	50	140	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	27945	95855.02	16.13	3.01×10^{-9}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	14.36	9.98	13.01	21.87	14.58

Crop	n	Mean	SD
Brinjal	47	153.74	22.08
Cotton	40	185.10	18.48
Okra	48	167.54	21.80
Soybean	35	152.43	33.33

Table 12. Morphometrics of puparia in the intraspecific populations – breadth of abdominal segment 1 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	14	11	14	26	12	14	16	14
2	15	16	15	15	27	13	15	14	18
3	0	17	14	15	28	13	18	15	15
4	14	12	15	15	29	12	16	16	15
5	14	11	12	17	30	13	16	13	15
6	17	12	13	15	31	16	15	16	0
7	12	14	15	15	32	15	15	15	15
8	16	15	15	13	33	14	15	16	15
9	14	17	16	13	34	12	16	16	13
10	16	17	14	12	35	14	15	12	10
11	11	16	15	15	36	12	15	16	14
12	10	14	15	16	37	10	15	13	15
13	12	14	15	10	38	0	15	15	14
14	12	15	16	0	39	12	12	16	15
15	16	15	15	15	40	10	15	16	14
16	14	17	15	14	41	11	0	16	0
17	12	14	16	15	42	11	0	16	0
18	12	17	16	16	43	10	0	16	0
19	14	14	14	0	44	10	0	16	0
20	12	15	16	15	45	12	0	14	0
21	14	14	13	14	46	12	0	14	0
22	12	16	15	15	47	12	0	15	0
23	12	17	15	14	48	11	0	15	0
24	12	15	16	0	49	11	0	14	0
25	12	15	10	0	50	12	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	153.89	51.30	20.58	2.14×10^{-11}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	14.10	10.13	9.64	10.80	11.14

Crop	n	Mean	SD
Brinjal	47	12.66	1.78
Cotton	40	15.00	1.52
Okra	49	14.76	1.42
Soybean	35	14.43	1.56

Table 13. Morphometrics of puparia in the intraspecific populations – length of abdominal segment 2 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	150	180	0	120	26	170	194	190	90
2	196	155	150	115	27	150	204	140	180
3	156	180	0	180	28	158	196	178	164
4	160	180	160	130	29	170	193	138	150
5	106	166	150	206	30	140	168	166	120
6	144	188	148	178	31	180	158	168	0
7	150	190	150	174	32	180	200	178	176
8	146	188	174	140	33	180	160	180	176
9	160	190	190	94	34	160	196	178	172
10	122	190	156	158	35	130	174	130	0
11	130	150	140	190	36	194	200	160	186
12	158	160	136	196	37	150	200	130	156
13	170	164	160	110	38	168	160	0	100
14	170	200	132	170	39	176	140	128	116
15	160	210	170	140	40	170	193	128	110
16	180	190	170	140	41	180	0	110	0
17	194	200	160	144	42	180	0	132	0
18	180	180	178	139	43	190	0	140	0
19	184	190	130	0	44	188	0	130	0
20	160	200	180	180	45	160	0	140	0
21	140	150	156	160	46	158	0	122	0
22	168	210	170	168	47	156	0	100	0
23	176	160	140	90	48	180	0	140	0
24	180	164	138	0	49	170	0	128	0
25	120	168	130	0	50	0	0	138	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	27072.30	9024	16.63	1.68×10^{-9}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	14.32	10.30	12.40	21.89	14.48

Crop	n	Mean	SD
Brinjal	47	149.79	21.46
Cotton	40	180.98	18.64
Okra	49	163.22	20.24
Soybean	35	149.09	32.63

Table 14. Morphometrics of puparia in the intraspecific populations – breadth of abdominal segment 2 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	11	10	13	26	11	11	14	12
2	0	12	12	12	27	10	12	12	12
3	0	11	11	11	28	11	15	12	10
4	11	11	13	13	29	10	12	12	10
5	10	12	8	13	30	11	12	11	10
6	14	13	11	12	31	12	10	13	0
7	10	12	12	12	32	12	14	13	13
8	13	15	11	13	33	11	12	14	12
9	12	15	15	11	34	10	14	13	11
10	12	10	13	12	35	10	13	10	8
11	10	11	12	11	36	11	14	13	12
12	10	11	11	12	37	9	14	11	12
13	11	12	12	10	38	0	12	11	10
14	11	12	12	11	39	8	11	13	12
15	14	15	13	11	40	9	13	14	11
16	11	13	13	13	41	10	0	14	0
17	11	15	15	10	42	7	0	14	0
18	11	11	14	14	43	10	0	13	0
19	11	11	12	0	44	10	0	14	0
20	10	12	15	13	45	9	0	13	0
21	12	11	11	11	46	9	0	11	0
22	10	14	14	11	47	10	0	12	0
23	12	11	12	12	48	10	0	13	0
24	10	11	14	0	49	9	0	12	0
25	10	11	10	0	50	10	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	101.25	33.75	17.37	7.29×10^{-10}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	12.76	12.10	11.85	10.64	11.92

Crop	n	Mean	SD
Brinjal	46	10.54	1.35
Cotton	40	12.30	1.49
Okra	49	12.41	1.47
Soybean	36	11.56	1.23

Table 15. Morphometrics of puparia in the intraspecific populations –
length of abdominal segment 3 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	176	140	104	26	180	188	160	88
2	140	150	194	102	27	140	200	150	0
3	0	174	150	170	28	177	196	150	160
4	150	178	156	140	29	130	182	164	150
5	148	156	102	200	30	150	160	130	110
6	140	190	130	186	31	160	150	180	0
7	148	190	150	170	32	176	196	172	170
8	164	180	140	164	33	178	156	174	174
9	180	180	158	92	34	164	196	150	176
10	150	190	122	156	35	130	148	126	0
11	140	146	128	190	36	160	196	180	174
12	134	160	152	188	37	126	196	140	152
13	158	164	160	106	38	0	156	168	116
14	130	200	160	164	39	120	136	166	120
15	170	206	160	136	40	130	190	170	110
16	170	170	170	130	41	110	0	176	0
17	160	200	188	138	42	130	0	170	0
18	172	180	170	136	43	140	0	184	0
19	120	180	176	0	44	126	0	180	0
20	170	190	156	176	45	138	0	150	0
21	150	144	134	170	46	120	0	156	0
22	160	200	160	162	47	98	0	148	0
23	130	150	170	88	48	138	0	170	0
24	130	160	176	0	49	120	0	164	0
25	124	168	120	0	50	130	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	24726.51	8242.17	15.66	5.15×10^{-9}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	14.13	11.15	12.42	22.23	14.71

Crop	n	Mean	SD
Brinjal	47	144.87	20.47
Cotton	40	175.70	19.60
Okra	49	157.14	19.51
Soybean	34	146.12	32.48

Table 16. Morphometrics of puparia in the intraspecific populations –
breadth of abdominal segment 3 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	11	10	13	26	10	11	11	11
2	10	12	14	11	27	10	13	11	0
3	0	11	11	10	28	10	13	11	11
4	10	10	12	10	29	10	13	12	10
5	9	12	8	14	30	11	12	10	9
6	15	14	11	12	31	11	10	13	0
7	9	13	11	11	32	10	13	11	12
8	13	12	10	13	33	10	12	12	11
9	10	13	14	9	34	10	14	12	11
10	11	13	10	12	35	8	11	9	7
11	10	12	10	11	36	9	12	11	11
12	10	12	10	12	37	7	15	11	11
13	10	11	11	9	38	0	11	11	9
14	10	13	11	11	39	7	11	12	11
15	12	14	11	10	40	7	13	13	10
16	10	15	13	13	41	8	0	13	0
17	10	13	14	10	42	7	0	13	0
18	10	15	13	14	43	10	0	13	0
19	10	13	12	0	44	10	0	13	0
20	10	13	14	12	45	10	0	11	0
21	11	11	10	11	46	8	0	11	0
22	10	13	11	10	47	6	0	12	0
23	11	11	12	11	48	8	0	13	0
24	10	10	12	0	49	8	0	12	0
25	9	11	9	0	50	9	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	164.96	54.99	26.16	6.36×10^{-14}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	16.34	10.92	12.02	13.47	13.09

Crop	n	Mean	SD
Brinjal	47	9.66	1.58
Cotton	40	12.30	1.34
Okra	49	11.53	1.39
Soybean	35	10.94	1.47

Table 17. Morphometrics of puparia in the intraspecific populations –
length of abdominal segment 4 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	170	140	100	26	170	180	150	83
2	140	140	190	100	27	140	198	140	174
3	0	172	150	162	28	163	186	140	138
4	140	170	154	152	29	130	174	160	140
5	142	150	100	206	30	150	142	120	124
6	136	188	120	178	31	158	148	172	0
7	140	188	140	174	32	174	186	166	166
8	160	170	140	184	33	178	156	162	170
9	180	170	158	88	34	160	186	144	170
10	140	180	122	150	35	124	120	120	0
11	130	140	120	180	36	150	194	176	154
12	126	158	148	180	37	120	186	136	150
13	150	150	150	104	38	0	156	156	110
14	120	190	150	160	39	114	130	166	124
15	170	200	150	130	40	128	180	160	116
16	160	160	160	140	41	90	0	170	0
17	154	190	176	136	42	130	0	160	0
18	164	180	160	136	43	132	0	180	0
19	118	160	174	164	44	120	0	176	0
20	160	180	142	170	45	130	0	140	0
21	140	140	130	164	46	116	0	150	0
22	150	194	150	162	47	90	0	134	0
23	120	150	160	83	48	136	0	160	0
24	120	158	172	0	49	118	0	154	0
25	120	160	118	0	50	130	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	19924.96	6641.65	12.63	1.74×10^{-7}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	15.15	12.02	12.67	21.67	15.26

Crop	n	Mean	SD
Brinjal	47	138.96	21.05
Cotton	40	168.25	20.23
Okra	49	150.33	19.05
Soybean	36	145.06	31.44

Table 18. Morphometrics of puparia in the intraspecific populations – breadth of abdominal segment 4 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	11	10	13	26	10	11	11	12
2	10	11	13	12	27	9	12	10	12
3	0	10	10	9	28	10	13	10	10
4	10	10	11	10	29	9	13	11	8
5	10	12	8	13	30	10	12	10	9
6	12	12	10	12	31	10	10	12	0
7	10	13	9	12	32	10	13	11	10
8	12	12	10	11	33	10	12	11	10
9	10	13	12	10	34	10	13	12	10
10	11	12	10	14	35	7	11	9	0
11	10	12	10	11	36	10	12	10	8
12	10	12	9	11	37	8	12	10	8
13	10	11	10	9	38	0	10	11	10
14	10	14	12	10	39	7	10	12	10
15	11	12	10	10	40	7	12	11	9
16	10	14	12	12	41	8	0	13	0
17	10	12	13	10	42	7	0	12	0
18	10	14	13	12	43	8	0	12	0
19	10	12	12	9	44	10	0	13	0
20	9	13	12	12	45	10	0	11	0
21	10	10	9	10	46	8	0	10	0
22	10	13	11	9	47	7	0	10	0
23	10	13	11	12	48	8	0	10	0
24	10	11	12	0	49	8	0	11	0
25	9	10	9	0	50	9	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	16532.36	3510.70	10.60	2.62×10^{-6}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.02	9.94	11.44	14.45	12.13

Crop	n	Mean	SD
Brinjal	47	9.44	1.23
Cotton	40	11.87	1.18
Okra	49	10.82	1.24
Soybean	36	34.67	49.89

Table 19. Morphometrics of puparia in the intraspecific populations –
length of abdominal segment 5 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	160	140	100	26	160	176	140	80
2	130	130	180	100	27	130	196	134	170
3	0	160	150	158	28	160	184	130	140
4	120	160	140	160	29	122	174	158	138
5	140	140	94	174	30	140	146	120	120
6	126	184	110	178	31	150	146	160	0
7	140	170	140	156	32	170	174	158	160
8	158	166	130	174	33	166	154	150	168
9	170	160	148	86	34	160	176	130	140
10	130	168	116	148	35	120	120	116	0
11	120	136	120	180	36	140	194	166	130
12	120	140	138	180	37	110	186	130	146
13	150	140	150	100	38	0	156	146	110
14	110	180	140	144	39	110	130	160	126
15	160	200	140	120	40	120	180	154	120
16	150	160	150	130	41	100	0	160	0
17	150	180	164	120	42	126	0	150	0
18	160	160	156	134	43	120	0	174	0
19	110	150	156	160	44	110	0	172	0
20	150	170	136	166	45	122	0	130	0
21	130	130	120	164	46	110	0	146	0
22	140	180	140	160	47	80	0	128	0
23	110	148	150	80	48	128	0	152	0
24	110	148	170	0	49	100	0	150	0
25	110	152	112	0	50	120	0	0	0

Summary: Single Factor ANOVA

Source	DF	ANOVA SS	Mean Square	F Value	P Value	F crit
CROP	3	26779.34	6926.45	14.11	3.02×10^{-08}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	16.27	12.36	12.73	21.01	15.45

Crop	n	Mean	SD
Brinjal	47	131.23	21.35
Cotton	40	161.40	19.97
Okra	49	142.94	18.20
Soybean	36	139.44	29.29

Table 20. Morphometrics of puparia in the intraspecific populations –
breadth of abdominal segment 5 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	10	10	13	26	10	10	11	10
2	11	9	12	12	27	8	11	10	14
3	0	10	13	9	28	11	11	10	10
4	9	10	10	11	29	10	13	11	8
5	9	11	8	14	30	10	10	10	7
6	12	11	10	12	31	9	9	12	0
7	9	12	10	11	32	10	12	11	12
8	11	12	10	11	33	10	10	10	12
9	11	12	12	9	34	9	12	11	12
10	10	11	10	13	35	9	11	9	10
11	10	11	10	10	36	10	10	10	7
12	10	10	9	10	37	8	12	10	11
13	10	10	10	8	38	0	10	10	11
14	10	13	12	10	39	7	10	11	0
15	10	10	10	10	40	8	11	11	10
16	10	12	12	12	41	6	0	11	9
17	10	12	13	10	42	6	0	11	0
18	10	12	12	12	43	10	0	11	0
19	10	11	11	8	44	9	0	11	0
20	10	12	10	11	45	8	0	11	0
21	10	9	8	9	46	8	0	10	0
22	10	11	10	7	47	8	0	10	0
23	10	12	10	10	48	9	0	10	0
24	9	10	11	0	49	9	0	10	0
25	9	10	8	0	50	9	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	54.20	18.66	10.51	2.25 x 10 ⁻⁶	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	12.87	9.81	10.52	17.61	12.78

Crop	n	Mean	SD
Brinjal	47	9.38	1.21
Cotton	40	10.88	1.07
Okra	49	10.47	1.10
Soybean	37	10.41	1.83

Table 21. Morphometrics of puparia in the intraspecific populations –
length of abdominal segment 6 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	156	126	100	26	150	170	138	78
2	120	120	176	90	27	120	176	120	160
3	0	150	130	146	28	154	178	120	134
4	128	150	130	146	29	120	170	154	130
5	138	130	86	180	30	130	134	110	116
6	120	160	110	184	31	148	130	152	0
7	126	164	128	156	32	164	166	144	150
8	150	156	120	164	33	168	146	140	164
9	160	160	134	80	34	156	166	120	130
10	120	154	100	144	35	110	130	114	0
11	110	124	100	150	36	130	180	150	80
12	116	132	120	178	37	110	184	120	140
13	140	138	150	99	38	0	144	138	116
14	100	170	130	130	39	100	126	152	124
15	150	180	132	110	40	110	180	140	124
16	140	150	140	126	41	90	0	156	0
17	140	170	154	110	42	120	0	144	0
18	150	150	146	130	43	110	0	164	0
19	100	140	150	144	44	100	0	160	0
20	140	160	122	160	45	118	0	120	0
21	120	120	110	160	46	106	0	132	0
22	130	170	130	156	47	78	0	118	0
23	100	140	146	78	48	120	0	140	0
24	100	138	160	0	49	94	0	140	0
25	100	140	110	0	50	118	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	18541.72	6186.57	12.62	1.76×10^{-7}	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	17.31	12.25	13.98	22.42	16.39

Crop	n	Mean	SD
Brinjal	47	123.87	21.45
Cotton	40	152.55	18.69
Okra	49	133.18	18.62
Soybean	36	132.42	29.69

Table 22. Morphometrics of puparia in the intraspecific populations –
breadth of abdominal segment 6 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	15	8	11	26	14	10	11	0
2	8	14	15	15	27	11	17	11	10
3	0	10	9	13	28	12	0	10	0
4	10	16	10	11	29	12	12	12	12
5	13	15	11	15	30	14	13	10	7
6	15	11	10	10	31	12	9	10	0
7	13	15	13	9	32	10	12	10	11
8	16	11	10	15	33	12	11	10	10
9	13	11	10	11	34	13	12	10	10
10	15	10	9	11	35	11	12	10	7
11	12	12	10	9	36	12	10	10	11
12	13	12	10	8	37	10	10	10	10
13	12	13	10	8	38	0	10	10	0
14	12	12	10	9	39	10	12	15	11
15	12	10	14	9	40	10	11	16	9
16	12	16	10	11	41	10	0	16	0
17	12	10	12	10	42	10	0	15	0
18	13	16	11	12	43	10	0	16	0
19	13	10	11	12	44	7	0	16	0
20	13	10	10	13	45	12	0	11	0
21	15	12	10	10	46	9	0	12	0
22	14	10	10	10	47	10	0	12	0
23	13	11	13	12	48	10	0	12	0
24	13	10	10	0	49	19	0	11	0
25	12	10	10	0	50	10	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	44.54	14.85	3.38	0.02	2.65

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	17.81	17.94	18.46	18.91	18.23

Crop	n	Mean	SD
Brinjal	47	12.00	2.14
Cotton	39	11.87	2.13
Okra	49	11.27	2.08
Soybean	34	10.65	2.01

Table 23. Morphometrics of puparia in the intraspecific populations –
length of abdominal segment 7 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	138	120	80	26	140	160	126	0
2	110	110	160	76	27	110	160	110	138
3	0	140	120	130	28	140	0	114	130
4	100	130	126	130	29	116	156	148	124
5	130	120	78	140	30	120	120	100	110
6	114	140	100	150	31	140	120	140	0
7	120	150	100	140	32	150	142	130	0
8	140	150	110	0	33	150	140	120	160
9	150	150	120	60	34	144	156	110	120
10	110	150	90	140	35	100	116	108	0
11	100	120	90	100	36	120	154	140	96
12	110	120	110	160	37	100	168	110	130
13	130	120	140	90	38	0	126	126	118
14	90	160	130	124	39	96	110	140	110
15	140	160	130	0	40	106	150	126	126
16	130	140	136	124	41	80	0	140	0
17	130	160	148	108	42	110	0	140	0
18	140	140	136	126	43	100	0	158	0
19	98	130	140	138	44	90	0	154	0
20	130	150	112	146	45	104	0	110	0
21	110	100	100	150	46	90	0	120	0
22	120	154	120	146	47	70	0	108	0
23	90	130	136	74	48	100	0	130	0
24	90	128	150	0	49	84	0	130	0
25	84	130	90	0	50	110	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	13448.20	4482.73	10.60	2.69×10^{-6}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	18.40	12.47	15.50	20.93	16.62

Crop	n	Mean	SD
Brinjal	47	113.53	20.89
Cotton	39	138.41	17.25
Okra	49	123.06	19.08
Soybean	32	121.69	25.47

Table 24. Morphometrics of puparia in the intraspecific populations – breadth of abdominal segment 7 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	10	10	13	26	10	8	9	14
2	6	6	10	9	27	10	9	9	14
3	0	9	6	8	28	10	0	9	0
4	12	10	9	8	29	9	10	9	8
5	9	10	8	10	30	8	9	9	9
6	11	8	9	11	31	10	8	9	0
7	9	10	8	12	32	9	10	9	0
8	9	10	9	0	33	9	10	9	10
9	9	0	9	6	34	10	11	9	9
10	9	9	9	12	35	7	10	8	7
11	9	9	9	9	36	9	10	9	8
12	10	10	9	8	37	9	10	9	10
13	9	9	9	7	38	0	9	9	0
14	10	10	9	9	39	9	10	9	11
15	9	10	10	0	40	8	10	10	10
16	10	9	9	9	41	7	0	9	0
17	8	10	9	0	42	7	0	9	0
18	9	9	10	11	43	10	0	9	0
19	10	9	10	10	44	10	0	9	0
20	10	9	9	9	45	9	0	9	0
21	10	9	9	8	46	8	0	9	0
22	10	9	9	8	47	9	0	9	0
23	10	9	9	8	48	8	0	10	0
24	10	9	10	0	49	9	0	10	0
25	10	9	8	0	50	9	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	4.93	1.64	1.19	0.3164	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.77	9.42	7.52	20.80	12.73

Crop	n	Mean	SD
Brinjal	47	9.17	1.08
Cotton	38	9.34	0.88
Okra	49	9.04	0.68
Soybean	31	9.52	1.98

Table 25. Morphometrics of puparia in the intraspecific populations –
length of abdominal segment 8 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	130	106	84	26	130	150	110	130
2	110	100	140	60	27	100	138	90	130
3	0	120	110	120	28	130	0	110	126
4	90	120	112	110	29	100	146	138	116
5	120	110	66	136	30	110	118	90	110
6	110	130	90	140	31	130	116	130	0
7	110	130	90	132	32	140	126	120	0
8	130	140	100	158	33	130	126	110	154
9	140	0	100	66	34	130	140	100	110
10	100	138	80	140	35	90	110	88	0
11	90	110	80	84	36	110	146	126	90
12	100	100	100	100	37	90	146	100	124
13	120	110	130	80	38	0	116	120	110
14	80	150	120	120	39	90	106	128	108
15	130	150	118	0	40	90	140	120	120
16	120	130	128	110	41	80	0	130	0
17	120	150	138	0	42	100	0	130	0
18	130	130	126	110	43	90	0	146	0
19	90	120	130	130	44	80	0	140	0
20	120	140	110	140	45	100	0	90	0
21	100	90	90	140	46	80	0	106	0
22	110	140	110	140	47	60	0	90	0
23	80	120	124	68	48	90	0	120	0
24	80	110	140	0	49	80	0	120	0
25	74	110	80	0	50	100	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	16858.85	3619	8.94	1.62×10^{-5}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	19.17	12.90	17.30	21.74	17.73

Crop	n	Mean	SD
Brinjal	47	103.91	19.92
Cotton	38	126.57	16.31
Okra	49	111.63	19.32
Soybean	33	115.03	25.01

Table 26. Morphometrics of puparia in the intraspecific populations –
breadth of abdominal segment 8 (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	7	6	12	26	6	6	6	10
2	0	8	8	10	27	5	6	6	10
3	0	6	7	8	28	6	0	6	0
4	7	7	8	10	29	6	8	6	7
5	8	7	6	8	30	6	6	6	6
6	8	6	6	13	31	6	6	6	0
7	8	6	6	13	32	6	8	6	0
8	7	8	6	13	33	6	7	6	20
9	6	0	6	8	34	6	7	6	20
10	7	8	6	13	35	6	6	5	0
11	7	6	6	7	36	6	8	6	20
12	6	7	6	10	37	6	8	6	18
13	6	6	6	6	38	0	7	6	18
14	6	8	6	9	39	6	7	7	18
15	6	8	7	0	40	5	8	7	18
16	6	6	6	6	41	5	0	7	0
17	6	6	6	0	42	6	0	6	0
18	6	6	8	10	43	6	0	6	0
19	6	6	7	8	44	6	0	6	0
20	6	6	7	8	45	6	0	6	0
21	6	6	6	8	46	6	0	6	0
22	6	6	6	8	47	6	0	6	0
23	6	6	6	5	48	6	0	6	20
24	5	7	6	0	49	5	0	6	0
25	6	7	6	0	50	6	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	698.57	232.86	46.57	9.3×10^{-22}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.04	12.42	9.55	42.16	30.35

Crop	n	Mean	SD
Brinjal	46	6.11	0.67
Cotton	38	6.79	0.84
Okra	49	6.24	0.60
Soybean	33	11.45	4.83

Table 27. Morphometrics of puparia in the intraspecific populations – length of caudal furrow (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	18	16	21	26	18	20	16	0
2	0	20	15	0	27	18	20	15	20
3	0	20	11	12	28	18	25	14	20
4	20	18	18	0	29	18	21	18	15
5	18	20	12	20	30	20	18	14	15
6	20	22	15	18	31	18	20	18	0
7	17	20	15	16	32	18	20	18	20
8	20	0	15	20	33	20	23	16	20
9	20	20	15	15	34	18	20	18	0
10	20	15	10	10	35	18	22	15	20
11	18	17	12	20	36	20	20	18	15
12	16	20	12	20	37	19	20	15	18
13	18	20	17	12	38	0	0	15	15
14	16	20	18	20	39	19	18	17	18
15	19	20	18	0	40	17	0	18	15
16	19	20	18	0	41	16	0	15	18
17	17	20	18	0	42	14	0	16	16
18	20	20	18	15	43	18	0	18	20
19	18	20	20	0	44	17	0	18	0
20	18	20	15	20	45	17	0	14	0
21	18	18	15	20	46	17	0	17	0
22	20	20	16	18	47	14	0	15	0
23	17	20	20	20	48	18	0	18	0
24	15	20	18	0	49	18	0	17	0
25	15	18	12	0	50	18	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	316.48	105.49	23.18	1.64×10^{-12}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	8.82	8.40	14.30	16.68	12.05

Crop	n	Mean	SD
Brinjal	46	17.93	1.58
Cotton	37	19.81	1.66
Okra	49	15.96	2.28
Soybean	32	17.56	2.93

Table 28. Morphometrics of puparia in the intraspecific populations –
breadth of caudal furrow at apex (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	4	3	5	26	4	5	3	0
2	0	5	3	0	27	5	4	3	5
3	0	4	3	5	28	5	5	3	5
4	3	3	3	0	29	4	4	3	5
5	5	5	3	5	30	5	4	3	5
6	4	3	4	5	31	4	5	3	0
7	5	4	3	5	32	4	5	3	0
8	4	0	3	5	33	5	4	3	5
9	4	3	3	5	34	4	5	3	5
10	4	3	3	4	35	4	4	3	0
11	4	3	3	5	36	5	4	3	4
12	4	3	3	5	37	4	4	3	4
13	4	3	3	4	38	0	0	3	4
14	4	3	3	5	39	4	4	3	4
15	4	3	3	0	40	4	0	3	4
16	4	3	3	0	41	4	0	3	4
17	4	3	4	0	42	5	0	3	4
18	4	3	3	5	43	4	0	3	4
19	4	3	3	0	44	4	0	3	4
20	5	3	3	5	45	4	0	3	4
21	4	3	3	5	46	4	0	3	4
22	5	3	3	4	47	4	0	3	4
23	4	3	3	5	48	5	0	3	4
24	5	5	4	0	49	4	0	3	4
25	5	5	3	0	50	4	0	0	4

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	55.72	18.57	65.01	7.5×10^{-28}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.53	21.70	7.91	11.18	13.81

Crop	n	Mean	SD
Brinjal	46	4.26	0.49
Cotton	37	3.78	0.82
Okra	49	3.06	0.24
Soybean	38	4.53	0.51

Table 29. Morphometrics of puparia in the intraspecific populations –
breadth of caudal furrow at middle (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	4	3	4	26	4	4	3	0
2	0	5	3	0	27	4	3	3	4
3	0	4	3	4	28	3	4	3	5
4	3	3	3	0	29	3	4	3	4
5	5	4	3	4	30	4	3	3	4
6	3	3	3	4	31	3	4	3	0
7	5	4	3	4	32	3	4	3	0
8	3	0	3	4	33	4	3	3	5
9	4	3	3	4	34	4	4	3	5
10	4	3	3	5	35	3	3	3	0
11	3	3	3	4	36	5	3	3	5
12	4	3	3	5	37	4	3	3	5
13	4	3	3	4	38	0	0	3	5
14	3	3	3	4	39	4	3	3	5
15	4	3	3	0	40	4	0	3	5
16	4	3	3	0	41	3	0	3	5
17	3	3	4	0	42	4	0	3	5
18	4	3	3	5	43	3	0	3	5
19	3	3	3	0	44	3	0	3	5
20	4	3	3	4	45	4	0	3	5
21	4	3	3	5	46	3	0	3	5
22	4	3	3	4	47	3	0	3	5
23	4	3	3	5	48	3	0	3	5
24	4	4	4	0	49	4	0	3	5
25	4	4	3	0	50	4	0	0	5

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	55.58	18.53	81.34	2.04×10^{-32}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	16.29	16.41	6.57	10.76	13.13

Crop	n	Mean	SD
Brinjal	46	3.67	0.60
Cotton	37	3.38	0.55
Okra	49	3.04	0.20
Soybean	38	4.61	0.50

Table 30. Morphometrics of puparia in the intraspecific populations –
breadth of caudal furrow at base (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	3	3	4	26	4	3	3	0
2	0	4	3	0	27	3	3	3	5
3	0	4	3	4	28	3	3	3	5
4	3	3	3	0	29	3	3	3	5
5	5	3	3	5	30	4	3	3	5
6	3	3	3	5	31	3	3	3	0
7	5	3	3	5	32	3	4	3	0
8	3	0	3	5	33	4	3	3	5
9	3	3	3	4	34	3	3	3	5
10	3	3	3	4	35	3	3	3	5
11	3	3	3	5	36	5	3	3	5
12	3	3	3	5	37	4	3	3	5
13	4	3	3	3	38	0	0	3	5
14	3	3	3	4	39	4	3	3	5
15	4	3	3	0	40	4	0	3	5
16	3	3	3	0	41	3	0	3	5
17	3	3	4	0	42	3	0	3	5
18	3	3	3	4	43	3	0	3	5
19	3	3	3	0	44	3	0	3	4
20	3	3	3	4	45	3	0	3	4
21	4	3	3	5	46	3	0	3	4
22	3	3	3	4	47	3	0	3	4
23	4	2	3	5	48	2	0	3	4
24	3	3	3	0	49	3	0	3	4
25	4	4	3	0	50	3	0	0	4

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	558.36	186.12	59.98	3.15×10^{-26}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	19.12	11.80	4.73	49.08	42.95

Crop	n	Mean	SD
Brinjal	46	3.35	0.64
Cotton	37	3.08	0.36
Okra	49	3.02	0.14
Soybean	36	7.58	3.72

Table 31. Morphometrics of puparia in the intraspecific populations –
length of operculum (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	14	12	12	26	12	13	12	0
2	0	11	13	0	27	13	15	11	14
3	0	15	11	11	28	13	14	11	13
4	12	14	14	0	29	11	13	14	11
5	15	15	11	15	30	13	14	11	12
6	13	12	11	0	31	12	11	13	0
7	12	12	11	15	32	13	14	14	0
8	15	0	12	14	33	12	13	12	18
9	15	14	13	13	34	13	14	14	15
10	15	15	11	0	35	11	14	10	0
11	13	11	12	14	36	11	15	12	18
12	12	13	12	16	37	0	15	12	15
13	12	13	13	13	38	0	13	12	14
14	14	14	13	12	39	10	14	14	16
15	12	15	13	0	40	10	0	15	17
16	13	15	15	0	41	11	0	12	18
17	12	14	13	0	42	11	0	14	17
18	12	15	16	0	43	11	0	14	16
19	12	14	14	0	44	10	0	13	15
20	12	14	16	13	45	11	0	14	16
21	12	12	12	15	46	12	0	12	16
22	12	14	14	15	47	10	0	11	15
23	12	13	12	15	48	11	0	13	18
24	11	11	15	0	49	10	0	13	0
25	13	11	10	0	50	11	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	152.81	50.94	22.12	4.79×10^{-12}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.09	9.70	11.51	13.45	11.56

Crop	n	Mean	SD
Brinjal	45	12.07	1.34
Cotton	38	13.50	1.31
Okra	49	12.69	1.46
Soybean	33	14.76	1.98

Table 32. Morphometrics of puparia in the intraspecific populations –
breadth of operculum at apex (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	19	15	14	26	15	18	15	0
2	0	14	17	0	27	15	18	15	16
3	0	15	13	15	28	17	18	14	20
4	16	16	17	0	29	14	18	16	18
5	15	17	14	19	30	15	18	11	14
6	15	16	15	0	31	15	18	16	0
7	15	17	12	18	32	15	15	16	0
8	15	0	15	20	33	16	18	14	16
9	15	17	15	15	34	16	18	17	19
10	16	17	15	0	35	15	18	15	0
11	15	16	15	19	36	15	0	15	20
12	15	15	12	22	37	0	0	14	18
13	16	17	15	15	38	0	0	15	15
14	15	18	15	15	39	14	0	17	18
15	17	18	15	0	40	10	0	15	18
16	17	18	15	0	41	10	0	12	20
17	15	18	17	0	42	14	0	14	18
18	15	18	15	0	43	12	0	14	14
19	15	18	16	0	44	12	0	13	17
20	15	18	12	19	45	15	0	14	14
21	18	16	15	20	46	12	0	12	17
22	15	18	16	16	47	9	0	11	17
23	15	17	15	16	48	12	0	13	19
24	13	15	14	0	49	11	0	13	0
25	17	17	12	0	50	12	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	296.74	98.91	31.45	5.62×10^{-16}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.64	7.16	10.95	12.64	11.36

Crop	n	Mean	SD
Brinjal	45	14.47	1.97
Cotton	34	17.12	1.23
Okra	49	14.45	1.53
Soybean	33	17.30	2.19

Table 33. Morphometrics of puparia in the intraspecific populations – breadth of operculum at middle (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	11	18	20	26	19	20	18	0
2	0	15	19	0	27	18	20	18	19
3	0	20	15	18	28	20	20	18	18
4	20	19	19	0	29	18	20	19	16
5	18	19	15	0	30	18	20	14	15
6	19	19	17	0	31	18	17	18	0
7	18	21	16	20	32	19	20	19	0
8	19	0	18	19	33	21	20	18	10
9	21	21	17	20	34	19	20	17	13
10	22	20	17	0	35	17	0	15	0
11	19	18	17	21	36	19	0	15	16
12	18	18	15	15	37	0	0	14	11
13	18	18	18	15	38	0	0	15	10
14	18	20	19	17	39	17	0	17	11
15	19	20	18	0	40	15	0	15	12
16	19	20	19	0	41	12	0	16	12
17	19	20	20	0	42	15	0	16	12
18	17	20	19	0	43	15	0	16	12
19	18	20	19	0	44	15	0	15	12
20	17	20	18	20	45	17	0	12	12
21	20	18	17	18	46	14	0	14	10
22	19	20	20	21	47	12	0	14	14
23	18	20	18	20	48	15	0	15	14
24	15	18	19	0	49	16	0	15	0
25	20	18	15	0	50	17	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	238.52	79.50	13.36	8.42 x 10 ⁻⁸	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	12.31	10.00	11.27	24.00	14.13

Crop	n	Mean	SD
Brinjal	45	17.71	2.18
Cotton	33	19.09	1.91
Okra	49	16.84	1.90
Soybean	32	15.41	3.70

Table 34. Morphometrics of puparia in the intraspecific populations –
breadth of operculum at base (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	13	12	15	26	11	16	12	0
2	0	13	15	0	27	10	15	10	14
3	0	14	10	14	28	11	14	10	15
4	12	13	12	0	29	10	15	12	12
5	11	11	10	17	30	12	14	10	13
6	12	12	11	0	31	12	12	12	0
7	11	16	10	13	32	10	14	12	0
8	11	0	12	15	33	11	15	12	15
9	11	15	12	12	34	11	15	12	14
10	12	15	12	0	35	11	0	17	0
11	11	13	12	16	36	12	0	19	10
12	11	15	11	15	37	0	0	17	11
13	12	14	12	17	38	0	0	18	10
14	11	14	12	14	39	11	0	22	12
15	12	15	12	0	40	9	0	19	12
16	11	15	12	0	41	8	0	19	12
17	12	15	13	0	42	10	0	22	12
18	11	16	12	0	43	10	0	22	12
19	11	16	11	0	44	10	0	19	12
20	11	15	11	15	45	10	0	18	12
21	12	12	11	15	46	10	0	18	12
22	12	13	11	15	47	8	0	16	12
23	11	14	11	14	48	10	0	17	12
24	9	12	12	0	49	9	0	18	0
25	10	12	10	0	50	11	0	0	0

Summary: Single Factor ANOVA

Source	DF	ANOVA SS	Mean Square	F Value	P Value	F crit
CROP	3	288.58	96.19	17.68	6.26×10^{-10}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	9.74	9.84	26.46	13.72	18.11

Crop	n	Mean	SD
Brinjal	45	10.76	1.05
Cotton	33	14.03	1.38
Okra	49	13.71	3.63
Soybean	33	13.36	1.83

Table 35. Morphometrics of puparia in the intraspecific populations –
length of lingula (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	9	9	13	26	11	12	11	0
2	0	10	10	0	27	10	12	10	14
3	0	12	10	11	28	10	13	10	12
4	9	11	10	0	29	10	13	13	12
5	9	11	10	14	30	10	16	9	12
6	13	11	8	0	31	11	12	12	0
7	11	15	9	10	32	10	14	13	0
8	13	0	10	15	33	10	12	11	0
9	11	11	11	11	34	10	14	10	15
10	11	15	10	0	35	9	0	9	14
11	9	10	10	12	36	10	0	10	0
12	11	10	9	8	37	0	0	9	10
13	9	11	11	12	38	0	0	12	11
14	8	15	10	0	39	0	0	11	10
15	9	12	11	0	40	8	0	12	15
16	10	12	11	0	41	7	0	12	12
17	10	12	13	0	42	9	0	11	12
18	11	12	11	0	43	10	0	12	12
19	0	12	11	0	44	10	0	11	12
20	10	12	10	11	45	10	0	12	12
21	9	12	9	11	46	9	0	10	11
22	11	12	11	11	47	7	0	10	12
23	10	12	10	11	48	8	0	10	12
24	8	11	10	0	49	9	0	11	10
25	9	10	9	0	50	9	0	0	12

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	144.09	48.03	24.96	3.24×10^{-13}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.15	13.42	11.03	13.27	12.72

Crop	n	Mean	SD
Brinjal	43	9.72	1.28
Cotton	33	12.06	1.62
Okra	49	10.49	1.16
Soybean	33	11.88	1.58

Table 36. Morphometrics of puparia in the intraspecific populations –
breadth of lingua at apex (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	7	6	8	26	10	9	9	0
2	0	5	7	0	27	8	9	7	8
3	0	10	6	8	28	9	10	9	10
4	9	8	7	0	29	8	9	8	7
5	8	8	6	10	30	9	9	8	6
6	9	8	7	0	31	9	8	9	0
7	7	10	6	8	32	9	9	8	0
8	9	0	6	9	33	9	9	8	0
9	9	9	8	7	34	8	9	9	9
10	9	9	8	0	35	8	0	8	0
11	9	8	7	9	36	9	0	8	9
12	7	8	8	10	37	0	0	7	8
13	8	8	8	11	38	0	0	9	8
14	7	10	8	0	39	0	0	8	9
15	8	10	8	0	40	7	0	9	9
16	9	10	8	0	41	6	0	8	9
17	10	10	8	0	42	7	0	8	7
18	8	10	9	0	43	7	0	9	7
19	0	10	9	0	44	7	0	9	7
20	8	10	7	8	45	9	0	8	7
21	9	8	7	5	46	7	0	7	7
22	8	8	8	9	47	8	0	7	7
23	8	10	9	9	48	7	0	8	7
24	8	8	9	0	49	7	0	8	7
25	9	8	7	0	50	8	0	0	7

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	20.39	6.79	6.06	6.00×10^{-4}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.39	12.82	11.87	16.10	12.94

Crop	n	Mean	SD
Brinjal	43	8.19	0.93
Cotton	33	8.82	1.13
Okra	49	7.82	0.93
Soybean	33	8.06	1.30

Table 37. Morphometrics of puparia in the intraspecific populations –
breadth of lingula at middle (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	4	5	9	26	7	7	6	0
2	0	6	5	0	27	6	7	6	7
3	0	7	5	6	28	7	8	6	8
4	7	7	6	0	29	6	7	6	6
5	6	7	5	8	30	6	7	6	5
6	7	7	6	0	31	7	6	7	0
7	5	8	5	7	32	7	7	6	0
8	6	0	5	7	33	7	7	6	0
9	7	8	6	6	34	6	7	6	8
10	7	8	6	0	35	6	0	6	0
11	6	7	6	6	36	7	0	6	8
12	5	7	6	8	37	0	0	6	7
13	6	6	6	7	38	0	0	7	7
14	6	8	6	0	39	0	0	6	8
15	6	8	6	0	40	6	0	6	8
16	6	8	6	0	41	4	0	6	7
17	8	8	6	0	42	6	0	6	7
18	6	8	7	0	43	6	0	6	6
19	0	8	7	0	44	6	0	6	6
20	6	8	6	7	45	7	0	6	6
21	7	6	6	5	46	6	0	5	6
22	6	6	6	7	47	6	0	5	6
23	6	8	7	8	48	6	0	6	6
24	6	6	6	0	49	5	0	6	6
25	6	6	6	0	50	6	0	0	6

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	32.61	16.67	17.72	6.22×10^{-10}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.42	13.22	8.70	14.41	12.06

Crop	n	Mean	SD
Brinjal	43	6.21	0.71
Cotton	33	7.06	0.93
Okra	49	5.94	0.52
Soybean	33	6.82	0.98

Table 38. Morphometrics of puparia in the intraspecific populations –
breadth of lingula at base (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	0	3	3	26	4	5	4	5
2	0	5	3	5	27	4	4	3	4
3	0	4	3	4	28	4	4	4	4
4	3	3	4	3	29	4	4	3	4
5	3	3	3	3	30	3	4	4	4
6	3	3	4	3	31	4	4	4	4
7	3	4	3	4	32	4	3	4	3
8	3	0	3	0	33	4	4	4	4
9	4	4	4	4	34	3	4	4	4
10	4	4	4	4	35	4	4	4	4
11	4	3	4	3	36	4	0	3	0
12	3	3	4	3	37	0	0	3	0
13	4	3	4	3	38	0	4	4	0
14	4	4	4	4	39	3	0	4	0
15	4	4	4	4	40	3	0	4	0
16	4	4	4	4	41	4	0	3	0
17	4	4	4	4	42	4	0	4	0
18	3	4	4	4	43	4	0	4	0
19	0	4	3	4	44	4	0	4	0
20	4	4	4	4	45	3	0	4	0
21	4	4	4	4	46	3	0	3	0
22	3	4	4	4	47	3	0	3	0
23	3	4	4	4	48	3	0	4	0
24	4	4	4	4	49	3	0	4	0
25	4	4	3	4	50	4	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	1.72	0.57	2.36	0.07	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.96	12.61	12.6	13.61	13.24

Crop	n	Mean	SD
Brinjal	44	3.59	0.49
Cotton	34	3.85	0.50
Okra	49	3.69	0.46
Soybean	34	3.82	0.52

Table 39. Morphometrics of puparia in the intraspecific populations –
breadth of caudal seta (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	2	1	2	26	2	2	0	2
2	0	2	1	0	27	0	2	1	2
3	0	2	0	2	28	1	2	1	2
4	0	2	1	2	29	1	2	1	2
5	1	2	1	2	30	1	2	1	2
6	1	2	1	2	31	1	2	1	0
7	1	2	1	2	32	1	2	1	0
8	1	2	1	2	33	1	2	1	0
9	1	2	1	2	34	1	2	1	2
10	1	2	1	2	35	1	0	1	2
11	1	2	1	2	36	1	0	0	2
12	1	2	1	2	37	0	0	1	2
13	1	2	1	2	38	1	0	1	2
14	1	2	1	2	39	0	0	1	2
15	1	2	0	0	40	1	0	1	2
16	1	2	1	0	41	1	0	1	2
17	2	2	1	0	42	1	0	1	2
18	1	2	1	2	43	1	0	1	2
19	1	2	1	0	44	1	0	1	2
20	1	2	1	2	45	1	0	1	2
21	2	2	1	2	46	1	0	1	2
22	1	2	1	0	47	1	0	1	2
23	2	2	0	2	48	1	0	1	2
24	2	2	1	0	49	0	0	1	0
25	2	2	1	0	50	0	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	33.87	11.29	335.06	9.26×10^{-67}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	30.70	0.00	0.00	0.00	12.29

Crop	n	Mean	SD
Brinjal	41	1.14	0.35
Cotton	34	2.00	0.00
Okra	44	1.00	0.00
Soybean	37	2.00	0.00

Table 40. Morphometrics of puparia in the intraspecific populations –
length of vasiform orifice (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	25	25	35	26	30	30	31	0
2	0	25	32	0	27	26	32	25	32
3	0	28	23	28	28	35	30	25	28
4	28	27	32	0	29	25	31	30	28
5	25	30	22	25	30	32	33	26	28
6	31	30	30	0	31	31	25	30	0
7	29	31	25	25	32	28	32	30	30
8	32	0	25	33	33	27	28	30	0
9	30	30	30	30	34	28	30	30	31
10	32	37	25	0	35	25	0	26	26
11	32	25	25	34	36	27	0	32	26
12	28	26	25	36	37	0	0	25	32
13	30	25	25	25	38	0	0	32	26
14	27	30	30	0	39	27	0	31	25
15	28	34	28	0	40	22	0	30	30
16	28	30	30	0	41	21	0	30	27
17	28	30	30	0	42	23	0	28	27
18	30	30	30	0	43	25	0	31	25
19	25	32	30	0	44	25	0	30	26
20	30	32	27	33	45	27	0	28	26
21	28	25	25	32	46	24	0	26	25
22	30	33	30	31	47	20	0	24	28
23	30	30	28	32	48	24	0	27	0
24	24	25	30	0	49	25	0	30	0
25	28	26	22	0	50	28	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	77.98	25.99	2.72	0.05	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.52	10.59	10.15	11.10	10.93

Crop	n	Mean	SD
Brinjal	45	27.51	3.17
Cotton	33	29.27	3.10
Okra	49	27.97	2.84
Soybean	32	29.90	3.32

Table 41. Morphometrics of puparia in the intraspecific populations –
breadth of vasiform orifice at apex (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	25	19	20	26	17	20	20	19
2	0	15	19	0	27	12	20	16	19
3	0	18	18	16	28	20	20	15	21
4	19	18	19	0	29	15	20	18	20
5	15	18	17	20	30	20	21	15	15
6	16	20	17	0	31	18	18	16	0
7	15	20	19	20	32	20	20	17	0
8	17	0	19	20	33	19	20	19	15
9	18	18	20	15	34	19	20	17	20
10	18	19	17	20	35	15	20	16	0
11	19	20	17	20	36	0	21	17	20
12	15	18	16	17	37	0	18	16	15
13	17	19	17	17	38	0	20	19	20
14	17	20	18	0	39	0	20	19	20
15	19	18	17	0	40	11	20	18	20
16	18	20	16	0	41	15	0	18	20
17	19	20	20	0	42	15	0	15	0
18	19	20	19	0	43	17	0	16	0
19	15	20	20	0	44	13	0	19	0
20	18	20	17	21	45	14	0	16	0
21	19	19	17	22	46	15	0	16	0
22	19	20	19	22	47	11	0	15	0
23	17	18	19	19	48	13	0	16	0
24	15	18	17	0	49	14	0	16	0
25	18	18	13	0	50	16	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	215.57	71.85	19.09	1.41 x 10 ⁻¹⁰	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	14.20	7.67	9.22	11.26	10.82

Crop	n	Mean	SD
Brinjal	43	16.53	2.43
Cotton	39	19.41	1.49
Okra	49	17.36	1.61
Soybean	27	19.00	2.14

Table 42. Morphometrics of puparia in the intraspecific populations –
breadth of vasiform orifice near apex (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	37	20	23	26	20	23	23	22
2	0	18	22	0	27	16	22	21	22
3	0	23	20	21	28	23	22	20	23
4	21	21	22	0	29	17	22	23	22
5	20	22	19	22	30	22	23	19	18
6	22	22	19	0	31	22	20	18	0
7	20	22	20	21	32	22	22	22	0
8	22	0	20	22	33	22	23	22	30
9	22	22	22	16	34	22	22	23	30
10	22	21	19	0	35	20	0	20	0
11	22	22	19	22	36	0	0	22	30
12	18	23	19	20	37	0	0	20	25
13	21	22	19	20	38	0	0	23	34
14	21	23	21	0	39	0	0	23	32
15	22	22	20	0	40	15	0	22	25
16	22	22	22	0	41	18	0	23	31
17	20	22	24	0	42	18	0	21	0
18	21	22	22	0	43	20	0	23	0
19	20	22	23	0	44	18	0	21	0
20	22	22	21	23	45	19	0	21	0
21	23	21	21	24	46	19	0	20	0
22	21	22	21	24	47	14	0	18	0
23	22	23	22	22	48	17	0	21	0
24	19	20	22	0	49	16	0	22	0
25	21	20	16	0	50	18	0	0	0

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	288.47	96.15	12.72	1.94×10^{-7}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	11.23	12.80	7.93	18.71	12.78

Crop	n	Mean	SD
Brinjal	43	20.04	2.25
Cotton	33	22.27	2.85
Okra	49	20.93	1.66
Soybean	26	24.00	4.49

Table 43. Morphometrics of puparia in the intraspecific populations –
breadth of vasiform orifice near base (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	20	16	20	26	12	19	18	18
2	0	15	16	0	27	10	19	12	20
3	0	22	17	20	28	15	18	14	15
4	14	15	16	0	29	12	18	20	16
5	13	21	15	21	30	18	18	12	16
6	14	20	15	0	31	15	16	19	0
7	13	21	16	18	32	16	18	18	0
8	16	0	15	19	33	18	21	18	0
9	16	19	16	11	34	18	18	16	15
10	16	16	15	0	35	17	0	14	10
11	17	15	14	15	36	0	0	15	22
12	12	21	14	15	37	0	0	14	19
13	18	20	15	18	38	0	0	17	18
14	13	22	16	0	39	0	0	17	20
15	17	20	14	0	40	12	0	17	16
16	15	19	18	0	41	14	0	15	18
17	15	19	17	0	42	14	0	14	14
18	16	19	18	0	43	15	0	15	18
19	14	19	18	0	44	12	0	16	16
20	16	19	18	19	45	12	0	12	17
21	15	18	15	17	46	12	0	12	19
22	17	20	18	20	47	10	0	14	20
23	15	17	14	18	48	11	0	14	17
24	14	17	19	0	49	11	0	12	17
25	12	16	11	0	50	14	0	0	18

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	421.12	140.37	28.22	1.24×10^{-14}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	6.39	9.46	7.36	6.75	13.71

Crop	n	Mean	SD
Brinjal	43	14.33	2.24
Cotton	33	18.64	1.97
Okra	49	15.53	2.11
Soybean	35	17.43	2.58

Table 44. Morphometrics of puparia in the intraspecific populations –
breadth of vasiform orifice at base (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	0	4	5	6	26	5	5	5	4
2	0	6	5	0	27	4	5	5	5
3	0	5	5	5	28	5	5	5	5
4	4	6	5	0	29	4	5	5	5
5	4	6	5	4	30	5	5	5	5
6	5	5	5	0	31	5	5	5	0
7	4	5	5	4	32	4	5	5	0
8	5	5	5	5	33	5	5	5	0
9	5	5	5	5	34	5	5	5	5
10	5	0	5	5	35	4	5	5	6
11	5	5	5	5	36	0	5	5	5
12	4	5	5	5	37	0	0	5	5
13	4	5	5	5	38	0	0	5	5
14	5	5	5	0	39	0	5	5	5
15	5	5	5	0	40	4	0	5	5
16	5	5	5	0	41	4	0	5	5
17	5	5	5	0	42	4	0	5	5
18	5	5	5	0	43	4	0	5	5
19	4	5	5	0	44	4	0	5	5
20	6	5	5	5	45	4	0	5	5
21	6	5	5	5	46	4	0	5	5
22	5	5	5	5	47	4	0	5	5
23	5	5	5	4	48	5	0	5	5
24	5	5	5	0	49	4	0	5	5
25	5	5	5	0	50	4	0	0	5

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	4.42	1.47	9.44	8.9×10^{-6}	2.66

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	All
CV	13.23	6.51	0.00	7.71	8.06

Crop	n	Mean	SD
Brinjal	44	4.64	0.61
Cotton	37	5.05	0.33
Okra	48	5.00	0.00
Soybean	34	4.91	0.38

Table 45. Single Factor ANOVA of length vs breadth ratios of puparia in the intraspecific populations

Character	F value	P value
Puparia	1.31	0.26
Abdominal segment 1	11.46	6.69×10^{-7}
Abdominal segment 2	7.40	1×10^{-4}
Abdominal segment 3	6.56	3×10^{-4}
Abdominal segment 4	6.98	1×10^{-4}
Abdominal segment 5	5.56	1×10^{-3}
Abdominal segment 6	3.36	1×10^{-2}
Abdominal segment 7	10.08	3.3×10^{-6}
Abdominal segment 8	23.75	3.7×10^{-13}
Caudal furrow	22.91	9.5×10^{-13}
Vasiform orifice	12.23	2.39×10^{-7}

Table 46. List of statistically significant and non-significant characters of adults (in the descending order of their F values)

A. Significant:

Character No.	Group	Character	F Value	P Value
17	G7	Length of head	338.78	2.86×10^{-77}
22	G7	Breadth of thorax	71.87	2.15×10^{-31}
21	G7	Length of thorax	39.37	5.86×10^{-20}
23	G7	Length of abdomen	32.49	4.31×10^{-17}
19	G7	Length of compound eye	12.59	1.46×10^{-7}
24	G7	Breadth of abdomen	11.68	4.48×10^{-7}
18	G7	Breadth of head	9.71	5.27×10^{-6}
15	G1	Length of proboscis	6.54	3.00×10^{-4}

B. Non-significant:

Character No.	Character	F Value	P Value
20	Breadth of compound eye	2.38	0.07
16	Breadth of proboscis	0.83	0.47

Table 47. List of statistically significant characters of adults (based on their location in the body)

Character No.	Group	Character	F Value	P Value
Head				
18	G7	Breadth	9.71	5.27×10^{-6}
17	G7	Length	338.78	2.86×10^{-77}
19	G7	Length of compound eye	12.59	1.46×10^{-7}
15	G1	Length of proboscis	6.54	3×10^{-4}
Thorax				
22	G7	Breadth	71.87	2.15×10^{-31}
21	G7	Length	39.37	5.86×10^{-20}
Abdomen				
24	G7	Breadth	11.68	4.48×10^{-7}
23		Length	32.49	4.31×10^{-17}

Table 48. Morphometrics of adults in the intraspecific populations – length of head (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	55	50	50	75	26	60	70	60	65
2	54	51	70	60	27	60	55	60	60
3	65	55	60	60	28	60	60	60	60
4	65	65	65	60	29	65	70	59	60
5	55	58	64	65	30	60	60	62	70
6	50	53	50	60	31	56	60	52	65
7	50	60	55	60	32	60	65	60	60
8	50	55	65	60	33	60	70	55	58
9	50	60	60	60	34	60	60	50	62
10	65	55	50	60	35	55	70	53	65
11	50	70	50	50	36	60	65	50	60
12	65	70	57	50	37	60	67	55	62
13	60	66	60	60	38	60	73	57	65
14	55	55	58	55	39	60	78	50	64
15	60	67	60	60	40	60	70	60	64
16	55	70	58	60	41	68	61	61	65
17	50	70	60	65	42	65	60	60	55
18	60	60	62	60	43	58	70	56	58
19	60	75	61	55	44	60	65	62	60
20	65	55	55	60	45	60	75	57	60
21	50	70	55	60	46	60	70	57	60
22	60	75	55	64	47	60	67	61	62
23	70	60	52	65	48	65	65	60	60
24	62	60	55	65	49	60	65	55	65
25	60	50	65	60	50	65	67	60	60

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	25761	8587.1	338.78	2.86×10^{-77}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	10.53	11.16	8.12	9.12	10.14

Crop	n	Mean	SD
Brinjal	50	37.66	3.97
Cotton	50	63.86	7.12
Okra	50	57.68	4.68
Soybean	50	39.40	3.59

Table 49. Morphometrics of adults in the intraspecific populations –
breadth of head (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	35	30	30	50	26	40	45	35	35
2	30	30	40	45	27	35	40	35	45
3	35	30	30	40	28	35	35	33	35
4	45	45	35	40	29	35	35	36	40
5	35	30	30	40	30	40	40	35	45
6	32	35	28	40	31	32	35	30	40
7	35	35	35	40	32	40	40	35	38
8	35	30	45	40	33	40	35	30	35
9	35	32	40	40	34	40	45	30	40
10	44	34	30	40	35	35	40	30	42
11	35	35	30	35	36	40	35	35	40
12	42	35	40	35	37	40	38	32	42
13	40	42	40	35	38	40	40	37	42
14	30	35	35	30	39	40	45	25	40
15	40	34	35	35	40	39	45	40	40
16	35	30	35	42	41	42	32	40	44
17	30	30	40	35	42	45	40	44	35
18	30	35	40	40	43	42	40	35	35
19	37	45	42	40	44	40	35	35	42
20	38	35	37	42	45	40	40	30	40
21	30	40	30	40	46	40	45	35	40
22	40	35	35	34	47	40	35	33	40
23	40	30	35	44	48	40	30	40	38
24	40	35	35	40	49	40	40	34	40
25	35	35	40	35	50	40	35	34	40

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	515.86	171.953	9.71	5.27×10^{-6}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	10.53	13.16	12.46	9.11	11.33

Crop	n	Mean	SD
Brinjal	50	37.66	3.96
Cotton	50	36.54	4.81
Okra	50	35.00	4.36
Soybean	50	39.40	3.59

Table 50. Morphometrics of adults in the intraspecific populations –
length of compound eye (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	27	23	22	18	26	30	30	26	25
2	22	27	25	20	27	30	22	24	26
3	27	20	27	20	28	30	24	24	25
4	23	23	28	20	29	26	26	26	25
5	24	25	27	25	30	25	25	29	29
6	25	24	25	25	31	26	28	25	26
7	30	26	25	20	32	26	26	21	26
8	30	25	26	20	33	25	26	22	25
9	25	26	21	22	34	28	27	24	25
10	24	27	24	23	35	25	22	24	24
11	22	28	22	20	36	28	25	22	28
12	26	38	26	21	37	23	30	24	25
13	25	26	26	19	38	25	26	25	24
14	27	32	25	23	39	25	25	20	27
15	27	28	28	25	40	28	27	23	25
16	25	28	24	25	41	28	26	25	25
17	28	32	25	25	42	27	25	24	25
18	27	27	27	23	43	25	25	25	22
19	26	30	24	24	44	20	25	25	25
20	28	25	25	24	45	25	28	25	24
21	29	35	23	24	46	25	25	26	24
22	30	26	25	24	47	28	25	20	25
23	28	23	25	24	48	26	25	27	22
24	27	22	26	25	49	26	24	20	26
25	25	25	25	22	50	28	24	25	25

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	237.1	79.04	12.59	1.46×10^{-7}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	8.60	12.26	8.36	9.81	9.94

Crop	n	Mean	SD
Brinjal	50	26.30	2.26
Cotton	50	26.24	3.22
Okra	50	24.54	2.05
Soybean	50	23.78	2.33

Table 51. Morphometrics of adults in the intraspecific populations –
breadth of compound eye (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	12	12	10	9	26	12	11	11	11
2	10	12	10	10	27	12	11	11	12
3	11	12	10	10	28	12	11	12	11
4	12	15	11	11	29	12	11	11	11
5	12	12	11	12	30	12	11	13	12
6	12	14	10	12	31	10	11	11	11
7	17	12	11	12	32	10	13	10	11
8	12	11	10	12	33	10	11	10	11
9	12	11	12	11	34	12	10	11	10
10	10	11	10	12	35	10	11	10	12
11	12	10	11	11	36	10	11	11	12
12	10	11	11	10	37	10	11	11	10
13	10	10	10	10	38	12	10	11	10
14	10	10	11	10	39	11	10	10	12
15	12	10	10	10	40	11	12	11	12
16	11	9	10	10	41	12	12	10	12
17	12	12	10	11	42	12	11	10	11
18	11	13	12	10	43	11	11	11	11
19	10	12	11	11	44	9	10	10	12
20	10	10	11	10	45	11	10	10	11
21	12	16	12	12	46	11	10	10	12
22	11	12	12	12	47	12	10	10	11
23	12	10	12	11	48	11	10	12	11
24	11	10	11	11	49	12	12	10	11
25	10	11	11	10	50	11	12	10	11

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	8.09	2.69	2.38	0.07	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	10.87	11.85	7.24	7.44	9.63

Crop	n	Mean	SD
Brinjal	50	11.24	1.22
Cotton	50	11.22	1.32
Okra	50	10.47	0.77
Soybean	50	11.02	0.82

Table 52. Morphometrics of adults in the intraspecific populations –
length of proboscis (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	60	65	62	55	26	65	65	66	65
2	62	66	65	50	27	70	65	50	72
3	68	74	60	60	28	70	63	69	72
4	76	72	55	70	29	72	73	62	72
5	72	75	76	60	30	63	70	70	72
6	69	60	80	65	31	70	70	70	60
7	72	72	70	68	32	70	68	60	65
8	74	62	65	70	33	62	66	70	60
9	68	67	58	60	34	80	60	60	60
10	65	65	53	70	35	70	60	60	67
11	65	55	67	60	36	60	67	54	72
12	70	63	61	60	37	70	75	63	64
13	70	77	63	52	38	65	65	60	65
14	72	65	70	60	39	72	72	54	65
15	70	75	58	65	40	75	78	70	68
16	67	67	60	65	41	75	65	65	68
17	70	70	75	60	42	70	64	62	72
18	60	68	63	65	43	60	63	62	65
19	80	70	82	55	44	70	70	60	68
20	65	55	57	65	45	70	64	62	70
21	62	75	60	65	46	60	65	68	72
22	60	72	60	65	47	65	60	42	65
23	65	75	58	74	48	60	50	64	65
24	65	70	57	65	49	60	70	63	60
25	80	66	65	72	50	65	70	70	60

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	728.66	242.88	6.54	3.00 x 10 ⁻⁴	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	8.12	8.76	11.50	8.56	9.26

Crop	n	Mean	SD
Brinjal	50	67.92	5.51
Cotton	50	67.18	5.88
Okra	50	63.12	7.25
Soybean	50	64.80	5.54

Table 53. Morphometrics of adults in the intraspecific populations –
breadth of proboscis (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	12	14	10	12	26	10	10	10	10
2	12	13	15	10	27	10	10	11	11
3	12	11	8	10	28	10	10	12	11
4	12	10	7	10	29	10	10	12	11
5	10	0	13	10	30	10	9	10	11
6	10	15	12	10	31	11	10	10	10
7	11	10	13	10	32	10	10	10	10
8	10	7	12	11	33	10	10	10	10
9	12	12	8	11	34	12	12	10	10
10	11	10	9	11	35	12	10	8	11
11	10	10	10	10	36	10	12	10	12
12	11	10	10	10	37	10	10	9	10
13	11	10	9	10	38	10	12	11	10
14	10	10	12	10	39	11	10	9	10
15	10	10	9	10	40	11	10	10	11
16	11	10	0	10	41	11	10	10	11
17	12	10	12	11	42	11	10	8	11
18	11	10	9	11	43	10	10	9	10
19	10	10	12	9	44	10	10	11	11
20	10	10	10	10	45	10	10	10	11
21	10	10	11	10	46	10	10	10	12
22	10	10	10	10	47	10	10	9	10
23	10	10	10	11	48	10	10	10	10
24	10	10	10	11	49	10	10	9	10
25	10	10	12	11	50	10	10	10	10

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	2.94	0.98	0.83	0.47	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	7.22	11.66	14.70	6.17	10.44

Crop	n	Mean	SD
Brinjal	50	10.54	0.76
Cotton	50	10.34	1.21
Okra	50	10.22	1.50
Soybean	50	10.46	0.64

Table 54. Morphometrics of adults in the intraspecific populations –
length of thorax (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	55	80	50	45	26	50	65	50	55
2	55	72	60	45	27	60	60	45	55
3	60	80	80	50	28	60	55	65	55
4	55	65	52	55	29	60	60	55	55
5	50	0	70	55	30	55	50	80	55
6	55	73	60	51	31	55	55	65	60
7	56	80	65	55	32	55	50	55	55
8	50	70	60	50	33	60	80	55	55
9	60	65	50	50	34	60	60	45	55
10	55	80	55	50	35	60	60	70	50
11	50	60	65	50	36	50	65	55	50
12	63	90	60	47	37	50	80	57	55
13	55	95	76	55	38	50	65	60	55
14	55	80	50	50	39	55	85	50	58
15	55	70	77	56	40	55	70	60	50
16	55	67	60	50	41	55	65	60	55
17	55	65	52	50	42	60	70	60	55
18	68	70	68	50	43	60	75	52	50
19	60	65	80	50	44	55	70	65	56
20	65	65	60	50	45	50	65	60	52
21	65	55	65	50	46	50	80	66	50
22	60	70	60	55	47	55	75	40	54
23	60	60	50	60	48	55	50	50	50
24	60	80	55	55	49	65	80	45	60
25	65	50	50	50	50	50	0	58	55

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	6900	2300	39.37	5.86×10^{-20}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	8.36	15.23	16.01	6.66	12.89

Crop	n	Mean	SD
Brinjal	50	56.64	4.73
Cotton	50	68.70	10.46
Okra	50	59.06	9.45
Soybean	50	52.78	3.51

Table 55. Morphometrics of adults in the intraspecific populations – breadth of thorax (observations calibrated to 312.5x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	40	55	45	40	26	45	80	45	45
2	40	0	55	35	27	50	55	40	45
3	45	70	75	40	28	50	50	58	45
4	40	70	40	45	29	55	55	50	45
5	42	0	60	45	30	45	45	73	45
6	40	52	50	40	31	45	45	50	50
7	40	70	55	45	32	42	45	50	45
8	40	60	50	40	33	50	70	50	45
9	44	65	45	40	34	55	55	40	47
10	42	65	60	40	35	45	50	60	40
11	42	70	60	40	36	40	60	50	40
12	50	78	55	35	37	40	60	52	45
13	47	80	65	45	38	40	60	55	45
14	45	70	45	40	39	45	75	42	47
15	45	65	63	45	40	45	60	53	42
16	45	65	55	40	41	40	60	55	45
17	40	70	45	40	42	50	50	55	43
18	55	75	66	40	43	50	60	46	40
19	52	70	60	40	44	45	65	60	45
20	50	55	55	40	45	40	60	55	45
21	50	60	60	40	46	44	60	55	40
22	50	75	55	45	47	45	60	36	45
23	52	55	45	55	48	45	45	45	40
24	45	75	50	45	49	55	68	45	50
25	55	45	45	45	50	40	0	50	45

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	10608	3536	71.87	2.15×10^{-31}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	10.7	15.46	15.66	8.53	13.81

Crop	n	Mean	SD
Brinjal	50	45.64	4.89
Cotton	50	61.88	9.57
Okra	50	52.58	8.24
Soybean	50	43.08	3.67

Table 56. Morphometrics of adults in the intraspecific populations –
length of abdomen (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	48	50	51	48	26	55	57	57	40
2	44	54	60	40	27	62	50	50	35
3	32	55	56	36	28	60	40	40	40
4	50	55	48	48	29	51	50	50	43
5	50	52	52	52	30	52	50	50	40
6	58	50	56	38	31	55	55	55	45
7	60	58	67	46	32	48	52	52	50
8	65	52	60	40	33	55	75	75	40
9	65	50	50	35	34	52	60	44	45
10	50	52	50	50	35	50	40	47	40
11	40	45	50	35	36	45	52	40	40
12	50	60	51	35	37	48	56	46	40
13	0	68	60	42	38	45	60	57	40
14	58	42	58	35	39	51	68	47	40
15	48	54	67	44	40	48	55	58	47
16	58	46	50	40	41	45	50	49	50
17	57	50	50	42	42	40	54	47	42
18	50	57	57	47	43	40	52	57	40
19	61	50	50	40	44	45	60	50	30
20	60	50	50	38	45	46	50	54	38
21	60	50	50	55	46	45	60	45	40
22	60	65	65	35	47	49	55	32	45
23	65	48	48	35	48	40	40	47	40
24	50	53	53	38	49	45	60	44	45
25	52	45	45	30	50	40	0	51	40

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	4608	1535.9	32.49	4.31 x 10 ⁻¹⁷	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	14.69	13.13	14.29	13.01	13.92

Crop	n	Mean	SD
Brinjal	50	51.08	7.50
Cotton	50	53.30	7.00
Okra	50	51.96	7.42
Soybean	50	41.18	5.36

Table 57. Morphometrics of adults in the intraspecific populations –
breadth of abdomen (observations calibrated to 125x)

S. No.	Brinjal	Cotton	Okra	Soybean	S. No.	Brinjal	Cotton	Okra	Soybean
1	17	16	22	26	26	25	30	24	25
2	23	23	23	15	27	31	30	16	20
3	12	38	24	25	28	34	20	25	20
4	25	25	15	20	29	28	20	22	20
5	20	30	25	31	30	32	24	22	32
6	30	15	25	15	31	28	23	17	15
7	34	38	24	26	32	24	22	31	25
8	32	22	20	23	33	30	36	25	20
9	30	24	24	20	34	30	30	16	20
10	25	25	15	20	35	25	25	26	28
11	20	28	16	15	36	20	30	16	28
12	22	36	28	12	37	33	28	25	25
13	0	41	33	25	38	25	36	30	20
14	20	28	25	25	39	22	36	15	25
15	20	27	27	24	40	35	27	26	24
16	27	33	21	22	41	34	28	21	25
17	25	21	25	25	42	20	32	22	24
18	30	33	31	25	43	29	28	24	22
19	28	28	28	20	44	25	22	24	25
20	25	25	25	20	45	25	22	24	15
21	30	26	19	18	46	24	32	20	28
22	30	32	24	15	47	26	22	13	26
23	30	22	15	27	48	25	20	27	22
24	20	20	21	20	49	15	25	16	20
25	26	20	21	10	50	25	0	25	20

Summary: Single Factor ANOVA

Source	DF	Anova SS	Mean Square	F Value	P Value	F crit
CROP	3	928.6	309.53	11.68	4.48×10^{-7}	2.69

Coefficient of Variation

	Brinjal	Cotton	Okra	Soybean	ALL
CV	19.69	21.97	21.02	21.42	21.11

Crop	n	Mean	SD
Brinjal	50	25.94	5.10
Cotton	50	27.02	5.94
Okra	50	22.56	4.74
Soybean	50	21.96	4.70

Table 58. Single Factor ANOVA of length vs breadth ratio of adults in the intraspecific populations

Character	F value	P value
Head	15.8	3.04×10^{-9}
Compound Eyes	6.17	4×10^{-4}
Proboscis	1108.60	1.6×10^{-120}
Thorax	16.29	1.7×10^{-9}
Abdomen	119.53	1.07×10^{-43}

Table 59. LSD difference of means of statistically significant characters of puparia

Character. No.	Character	Brinjal	Cotton	Okra	Soybean
1	Length	a	b	c	c
2	Breadth at apex	a	b	c	d
3	Breadth at middle	a	b	c	c
4	Breadth at base	a	b	a	c
5	Submargin	a	b	c	d
6	Length of abdominal segment 1	a	b	c	a
7	Breath of abdominal segment 1	a	b	b	b
8	Length of abdominal segment 2	a	b	c	a
9	Breath of abdominal segment 2	a	b	b	c
10	Length of abdominal segment 3	a	b	c	a
11	Breath of abdominal segment 3	a	b	c	ac
12	Length of abdominal segment 4	a	a	a	b
13	Breath of abdominal segment 4	a	a	a	b
14	Length of abdominal segment 5	a	b	b	b
15	Breath of abdominal segment 5	a	b	b	b
16	Length of abdominal segment 6	a	b	c	ac
17	Breath of abdominal segment 6	a	a	ab	b
18	Length of abdominal segment 7	a	b	c	ac
20	Length of abdominal segment 8	a	b	ac	c
21	Breath of abdominal segment 8	a	a	ac	bc
22	Length of caudal furrow	a	b	c	a
23	Breadth of caudal furrow at apex	a	b	c	d
24	Breadth of caudal furrow at middle	a	b	a	d
25	Breadth of caudal furrow at base	a	a	a	b
26	Length of operculum	a	b	c	d
27	Breadth of operculum at apex	a	b	a	b
28	Breadth of operculum at middle	a	b	a	c
29	Breadth of operculum at base	a	b	b	b
30	Length of lingula	a	b	c	b
31	Breadth lingula at apex	a	b	a	a
32	Breadth of lingula at middle	a	b	a	b
34	Breadth of caudal setae	a	b	c	b
35	Length of vasiform orifice	a	b	b	b
36	Breadth 1 of vasiform orifice at apex	a	b	c	b
37	Breadth 2 of vasiform orifice near apex	a	b	a	c
38	Breadth 3 of vasiform orifice near base	a	b	c	d
39	Breadth 4 of vasiform orifice at base	a	b	b	b

Table 60. LSD differences of means of statistically significant characters of adults

Character No.	Character	Brinjal	Cotton	Okra	Soybean
17	Length of head	c	a	b	c
18	Breadth of head	b	bc	c	a
19	Length of compound eyes	a	a	b	b
15	Length of proboscis	a	ab	c	bc
21	Length of thorax	b	a	b	c
22	Breadth of thorax	c	a	b	c
23	Length of abdomen	a	a	a	b
24	Breadth of abdomen	a	a	b	b

Table 61a. Correlation coefficients of significant characters of puparia from brinjal population

	1	2	3	4	5	6	7	8	9	10
1	1									
2	0.29	1								
3	*** 0.39	*** 0.74	1							
4	0.30	*** 0.99	*** 0.76	1						
5	0.13	** 0.34	0.26	*** 0.31	1					
6	** 0.35	*** 0.78	*** 0.82	*** 0.78	* 0.33	1				
7	*** 0.42	*** 0.46	*** 0.57	*** 0.47	0.24	*** 0.41	1			
8	* 0.34	*** 0.76	*** 0.84	*** 0.77	* 0.31	*** 0.97	*** 0.45	1		
9	*** 0.42	*** 0.50	*** 0.57	*** 0.51	0.15	*** 0.49	*** 0.75	*** 0.53	1	
10	* 0.29	*** 0.73	*** 0.81	*** 0.73	* 0.29	*** 0.96	*** 0.42	*** 0.98	*** 0.51	1
11	*** 0.45	*** 0.48	*** 0.56	*** 0.48	0.16	*** 0.52	*** 0.63	*** 0.54	*** 0.82	*** 0.49
12	* 0.30	*** 0.72	*** 0.82	*** 0.73	0.26	*** 0.94	*** 0.46	*** 0.97	*** 0.50	*** 0.98
14	0.28	*** 0.66	*** 0.78	*** 0.67	0.27	*** 0.91	*** 0.43	*** 0.94	*** 0.47	*** 0.96
15	*** 0.47	*** 0.55	*** 0.57	*** 0.55	-0.05	*** 0.59	*** 0.48	*** 0.60	*** 0.75	*** 0.57
16	0.26	*** 0.67	*** 0.80	*** 0.68	0.26	*** 0.90	*** 0.45	*** 0.93	*** 0.45	*** 0.95
17	*** 0.39	0.18	* 0.29	0.18	-0.04	* 0.31	* 0.29	** 0.35	*** 0.38	* 0.29
18	* 0.29	*** 0.63	*** 0.77	*** 0.64	0.26	*** 0.88	*** 0.45	*** 0.91	*** 0.45	*** 0.93
19	*** 0.39	** 0.29	* 0.29	** 0.29	-0.01	* 0.30	0.11	0.25	** 0.37	0.21
20	0.27	*** 0.62	*** 0.76	*** 0.63	* 0.30	*** 0.87	*** 0.49	*** 0.91	*** 0.47	*** 0.92
21	* 0.33	0.24	0.25	0.27	-0.01	0.21	*** 0.43	0.20	* 0.33	0.19
22	0.26	*** 0.52	*** 0.65	*** 0.55	0.15	*** 0.61	*** 0.47	*** 0.62	*** 0.48	*** 0.58
23	0.02	0.16	0.07	0.16	0.07	0.15	-0.11	0.12	-0.22	0.14
24	0.16	0.21	0.18	0.20	0.19	0.27	-0.10	0.22	-0.16	0.22
25	0.18	0.13	0.03	0.12	0.22	0.15	0.01	0.10	0.03	0.12
26	*** 0.60	* 0.31	*** 0.53	* 0.32	0.18	*** 0.48	*** 0.57	*** 0.51	*** 0.52	*** 0.50
27	*** 0.61	*** 0.49	*** 0.63	*** 0.49	* 0.35	*** 0.66	*** 0.52	*** 0.65	*** 0.46	*** 0.64
28	*** 0.67	*** 0.51	*** 0.70	*** 0.53	0.15	*** 0.69	*** 0.56	*** 0.70	*** 0.54	*** 0.67
29	*** 0.44	*** 0.53	*** 0.60	*** 0.54	* 0.35	*** 0.64	*** 0.50	*** 0.62	*** 0.52	*** 0.59
30	* 0.39	* 0.32	*** 0.60	0.35	0.07	*** 0.54	*** 0.45	*** 0.60	*** 0.48	*** 0.55
33	* 0.39	*** 0.52	*** 0.61	*** 0.54	0.20	*** 0.55	*** 0.56	*** 0.62	*** 0.51	*** 0.60
32	0.12	*** 0.53	*** 0.54	*** 0.55	0.10	*** 0.49	*** 0.46	*** 0.51	*** 0.39	*** 0.52
31	0.16	0.19	0.09	0.17	* 0.31	0.16	0.09	0.16	0.15	0.24
38	* 0.36	*** 0.48	*** 0.58	*** 0.46	*** 0.41	*** 0.61	** 0.37	*** 0.61	*** 0.41	*** 0.59
39	0.25	* 0.32	0.29	* 0.31	-0.08	* 0.31	0.17	* 0.32	** 0.37	0.28
34	0.21	0.18	0.05	0.17	-0.02	0.14	-0.01	0.17	0.29	0.19
35	*** 0.27	*** 0.33	*** 0.32	*** 0.32	* 0.03	*** 0.39	*** 0.22	*** 0.43	*** 0.46	*** 0.43
36	*** 0.38	*** 0.34	*** 0.28	*** 0.34	*** 0.03	*** 0.42	*** 0.23	*** 0.42	*** 0.44	*** 0.42
37	*** 0.37	*** 0.29	*** 0.22	*** 0.29	*** -0.02	*** 0.35	*** 0.26	*** 0.35	*** 0.45	*** 0.35
13	*** 0.41	*** 0.48	*** 0.46	*** 0.47	0.08	*** 0.58	*** 0.59	*** 0.61	*** 0.77	*** 0.58

Contd.....

Table 61b. Correlation coefficients of significant characters of puparia from brinjal population

	11	12	14	15	16	17	18	19	20	21
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11	1									
12	*** 0.49	1								
14	*** 0.45	*** 0.97	1							
15	*** 0.74	*** 0.57	*** 0.50	1						
16	*** 0.43	*** 0.97	*** 0.98	*** 0.47	1					
17	*** 0.45	0.26	0.23	*** 0.42	0.20	1				
18	*** 0.44	*** 0.95	*** 0.98	*** 0.48	*** 0.98	0.24	1			
19	*** 0.44	0.16	0.06	*** 0.33	0.10	0.30	0.08	1		
20	*** 0.47	*** 0.94	*** 0.97	*** 0.49	*** 0.97	0.26	*** 0.99	0.04	1	
21	0.39	0.18	0.19	** 0.37	0.22	0.18	0.22	0.23	0.23	1
22	0.47	*** 0.59	*** 0.53	*** 0.53	*** 0.54	* 0.32	*** 0.53	0.21	0.54	0.30
23	-0.11	0.15	0.18	-0.04	0.13	0.09	0.13	-0.18	0.11	-0.02
24	-0.12	0.22	0.21	-0.09	0.18	* 0.29	0.22	-0.02	0.22	0.09
25	-0.07	0.11	0.13	-0.02	0.10	0.11	0.15	-0.03	0.13	0.27
26	*** 0.54	*** 0.48	*** 0.50	*** 0.51	*** 0.49	*** 0.39	*** 0.48	0.21	*** 0.49	*** 0.49
27	*** 0.57	*** 0.62	*** 0.60	*** 0.51	*** 0.58	* 0.35	*** 0.56	*** 0.39	*** 0.56	** 0.35
28	*** 0.58	*** 0.68	*** 0.61	*** 0.65	*** 0.62	*** 0.45	*** 0.60	*** 0.42	*** 0.58	*** 0.39
29	*** 0.59	*** 0.58	*** 0.54	*** 0.58	*** 0.53	* 0.31	*** 0.53	** 0.32	*** 0.54	*** 0.48
30	*** 0.72	*** 0.57	*** 0.55	*** 0.63	*** 0.53	*** 0.45	*** 0.57	* 0.34	*** 0.59	*** 0.46
33	*** 0.48	*** 0.59	*** 0.52	*** 0.54	*** 0.54	* 0.31	*** 0.51	* 0.30	*** 0.51	0.26
32	* 0.35	*** 0.54	*** 0.45	*** 0.44	*** 0.49	0.02	*** 0.44	0.26	*** 0.42	0.19
31	0.08	0.21	0.21	0.10	0.16	-0.20	0.17	-0.04	0.16	-0.27
38	*** 0.41	*** 0.56	*** 0.59	*** 0.41	*** 0.57	0.20	*** 0.56	-0.06	*** 0.56	0.16
39	0.26	0.27	0.26	*** 0.38	0.26	0.29	0.26	0.33	0.25	0.05
34	0.25	0.12	0.16	0.22	0.08	0.25	0.09	0.12	0.06	0.00
35	*** 0.45	*** 0.38	*** 0.38	*** 0.30	*** 0.35	*** 0.47	*** 0.35	0.45	*** 0.32	0.27
36	*** 0.46	*** 0.39	*** 0.39	*** 0.31	*** 0.39	*** 0.37	*** 0.35	0.33	*** 0.31	0.14
37	*** 0.48	*** 0.32	*** 0.33	*** 0.29	*** 0.32	*** 0.38	*** 0.29	0.35	*** 0.26	0.20
13	*** 0.89	*** 0.55	*** 0.52	*** 0.73	*** 0.51	*** 0.45	0.51	*** 0.43	*** 0.54	0.47

Table 61c. Correlation coefficients of significant characters of puparia from brinjal population

	22	23	24	25	26	27	28	29	30	33
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										
14										
15										
16										
17										
18										
19										
20										
21										
22	1									
23	-0.12	1								
24	0.12	*** 0.45	1							
25	0.11	0.27	*** 0.71	1						
26	** 0.37	0.08	0.08	0.05	1					
27	*** 0.40	0.10	0.25	0.25	*** 0.58	1				
28	*** 0.59	0.01	0.24	0.23	*** 0.65	*** 0.86	1			
29	*** 0.64	-0.05	0.19	0.26	*** 0.45	*** 0.76	*** 0.75	1		
30	*** 0.58	-0.02	0.09	0.03	*** 0.45	*** 0.46	*** 0.57	*** 0.56	1	
33	*** 0.44	-0.06	0.03	0.13	*** 0.42	*** 0.61	*** 0.71	*** 0.55	0.44	1
32	* 0.35	-0.10	-0.11	0.00	0.25	*** 0.45	*** 0.57	*** 0.51	0.33	0.80
31	-0.11	0.09	-0.13	-0.06	0.08	0.24	0.21	0.07	-0.14	0.21
38	*** 0.53	-0.01	0.06	0.11	** 0.36	*** 0.51	*** 0.47	*** 0.59	0.27	0.34
39	0.25	-0.12	-0.12	-0.26	0.09	0.21	0.13	0.27	0.23	-0.02
34	-0.33	0.18	0.00	0.13	0.13	0.24	0.11	0.05	0.02	0.30
35	*** 0.26	0.08	-0.01	-0.07	*** 0.59	*** 0.69	*** 0.75	*** 0.74	*** 0.69	*** 0.61
36	*** 0.04	-0.05	-0.25	-0.32	*** 0.49	*** 0.40	*** 0.36	*** 0.25	* 0.22	*** 0.30
37	*** 0.01	-0.04	-0.25	-0.31	*** 0.51	*** 0.37	*** 0.31	*** 0.20	*** 0.25	*** 0.22
13	*** 0.46	-0.04	0.08	0.09	*** 0.64	*** 0.63	*** 0.68	*** 0.62	*** 0.67	*** 0.55

Contd.....

Table 61d. Correlation coefficients of significant characters of puparia from brinjal population

	32	31	38	39	34	35	36	37	13
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
33									
32	1								
31	0.24	1							
38	0.22	0.21	1						
39	0.00	-0.14	0.08	1					
34	0.25	0.22	0.12	0.14	1				
35	*** 0.39	0.06	*** 0.54	0.35	0.40	1			
36	*** 0.16	0.17	*** 0.77	0.37	0.48	*** 0.80	1		
37	*** 0.10	0.13	*** 0.76	0.39	0.50	*** 0.80	*** 0.98	1	
13	** 0.37	0.04	*** 0.40	* 0.34	0.28	*** 0.71	*** 0.61	*** 0.62	1

Table 62a. Correlation coefficients of significant characters of puparia from cotton population

	1	2	3	4	5	6	7	8	9	10
1	1									
2	0.04	1								
3	0.03	* 0.38	1							
4	0.14	*** 0.66	*** 0.48	1						
5	-0.12	0.11	-0.09	-0.10	1					
6	0.01	0.33	*** 0.83	* 0.40	-0.20	1				
7	0.27	0.29	0.19	0.09	-0.18	0.18	1			
8	0.01	* 0.39	*** 0.83	*** 0.46	-0.23	*** 0.95	0.20	1		
9	0.03	*** 0.48	*** 0.57	*** 0.56	0.10	*** 0.52	0.17	*** 0.60	1	
10	-0.03	* 0.39	*** 0.77	*** 0.44	-0.24	*** 0.90	0.15	*** 0.96	*** 0.55	1
11	* 0.24	* 0.39	*** 0.68	* 0.33	-0.14	*** 0.60	0.29	*** 0.62	*** 0.51	*** 0.61
12	-0.04	* 0.35	*** 0.70	** 0.41	-0.25	*** 0.80	0.13	*** 0.88	*** 0.46	*** 0.96
14	-0.02	* 0.42	*** 0.72	*** 0.50	-0.21	*** 0.81	0.15	*** 0.88	*** 0.53	*** 0.93
15	0.22	0.14	*** 0.60	* 0.33	0.04	*** 0.55	0.25	*** 0.56	*** 0.40	*** 0.50
16	-0.06	* 0.44	*** 0.78	*** 0.50	-0.10	0.85	0.19	*** 0.90	*** 0.60	*** 0.92
17	0.10	-0.11	0.06	-0.15	0.15	*** -0.03	-0.15	-0.07	-0.14	-0.08
18	0.04	* 0.38	*** 0.74	*** 0.47	-0.21	0.83	0.24	*** 0.89	*** 0.52	*** 0.90
19	0.04	0.07	0.27	0.30	0.27	0.27	-0.18	0.29	* 0.38	0.29
20	0.07	0.30	*** 0.73	*** 0.46	-0.20	0.83	0.20	*** 0.87	*** 0.53	*** 0.86
21	-0.09	* 0.37	0.17	0.30	0.31	0.25	0.02	0.21	0.31	0.26
22	0.03	** 0.40	*** 0.45	*** 0.42	0.27	0.22	0.12	0.24	*** 0.49	0.19
23	-0.23	0.16	-0.18	-0.03	* 0.34	-0.17	-0.02	-0.12	-0.01	-0.11
24	-0.08	0.06	-0.22	-0.22	0.19	-0.21	0.06	-0.11	-0.10	-0.07
25	-0.25	0.30	-0.11	0.01	-0.10	-0.15	0.05	0.00	0.02	0.04
26	0.12	0.29	*** 0.53	*** 0.43	0.04	*** 0.53	0.11	*** 0.56	* 0.37	*** 0.49
27	0.24	-0.17	* 0.37	*** 0.04	-0.09	*** 0.50	0.11	*** 0.44	0.19	* 0.34
28	0.18	*** 0.46	*** 0.52	0.65	0.07	*** 0.42	0.22	*** 0.46	* 0.35	** 0.42
29	0.25	* 0.35	*** 0.45	0.30	-0.14	*** 0.48	* 0.36	*** 0.49	0.18	*** 0.47
30	0.23	0.25	* 0.38	* 0.37	0.20	*** 0.39	0.28	* 0.40	0.15	* 0.40
33	0.31	0.25	*** 0.52	*** 0.52	-0.14	*** 0.48	0.31	*** 0.53	0.26	*** 0.48
32	* 0.40	* 0.36	*** 0.51	*** 0.49	0.06	*** 0.42	0.27	** 0.42	0.31	* 0.38
31	0.21	0.25	0.05	-0.06	-0.24	0.13	*** 0.45	0.15	0.00	0.07
38	-0.17	0.14	* 0.40	0.26	0.06	0.22	-0.20	* 0.33	0.24	0.33
39	0.05	0.23	-0.11	0.03	*** 0.44	-0.15	-0.27	-0.18	-0.04	-0.18
34	0.04	-0.12	-0.09	-0.07	-0.33	0.05	0.14	0.07	-0.15	0.12
35	0.04	-0.07	*** 0.05	*** -0.24	-0.25	*** 0.18	0.18	0.20	-0.18	*** 0.23
36	-0.23	-0.16	0.09	-0.55	0.06	0.07	-0.02	0.06	-0.24	0.07
37	0.00	** -0.23	-0.07	-0.36	-0.26	0.05	0.10	0.07	-0.27	0.12
13	-0.14	0.23	*** 0.63	0.24	0.03	0.58	*** 0.41	*** 0.56	*** 0.42	*** 0.51

Contd.....

Table 62b. Correlation coefficients of significant characters of puparia from cotton population

	11	12	14	15	16	17	18	19	20	21
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11	1									
12	*** 0.57	1								
14	*** 0.56	*** 0.96	1							
15	*** 0.64	*** 0.43	*** 0.41	1						
16	*** 0.55	*** 0.91	*** 0.96	*** 0.49	1					
17	0.15	-0.07	-0.13	0.11	-0.13	1				
18	*** 0.58	*** 0.89	*** 0.92	*** 0.60	*** 0.95	-0.16	1			
19	0.17	0.25	0.26	*** 0.43	* 0.38	0.05	* 0.34	1		
20	*** 0.55	*** 0.83	*** 0.89	*** 0.58	*** 0.92	-0.17	*** 0.96	0.32	1	
21	0.14	0.25	0.30	0.11	0.34	-0.15	0.29	0.28	0.28	1
22	0.21	0.18	0.23	0.19	0.31	-0.07	0.20	0.04	0.18	-0.11
23	-0.28	-0.10	-0.05	-0.25	-0.03	-0.04	-0.09	-0.10	-0.13	0.25
24	-0.24	-0.04	-0.09	-0.19	-0.08	0.06	-0.11	-0.30	-0.16	0.24
25	-0.05	0.01	-0.06	-0.25	-0.08	-0.03	-0.10	-0.26	-0.20	0.27
26	*** 0.47	0.42	*** 0.44	* 0.36	*** 0.50	0.20	*** 0.47	*** 0.47	*** 0.50	0.15
27	0.29	0.25	* 0.36	* 0.33	*** 0.44	0.03	*** 0.46	* 0.34	*** 0.60	-0.22
28	*** 0.45	* 0.40	** 0.42	*** 0.54	** 0.42	-0.17	*** 0.47	0.26	* 0.41	-0.15
29	*** 0.52	*** 0.43	* 0.40	*** 0.45	*** 0.48	0.05	*** 0.58	0.23	*** 0.55	-0.06
30	* 0.34	0.33	* 0.36	** 0.42	* 0.37	-0.05	* 0.37	0.28	* 0.43	0.12
33	*** 0.45	*** 0.48	** 0.50	*** 0.60	*** 0.53	-0.14	*** 0.57	*** 0.46	*** 0.56	-0.24
32	*** 0.58	* 0.35	* 0.37	*** 0.61	* 0.36	-0.06	** 0.43	0.19	** 0.42	-0.04
31	0.02	0.05	0.10	-0.09	0.15	-0.21	0.23	* -0.41	0.26	0.01
38	0.30	* 0.37	0.31	0.24	* 0.35	0.04	* 0.36	* 0.38	0.30	-0.12
39	-0.09	-0.18	-0.21	-0.13	-0.27	0.24	-0.27	-0.26	-0.27	0.18
34	0.04	0.15	0.01	0.08	-0.11	0.21	0.03	-0.25	-0.03	-0.28
35	*** 0.19	0.25	*** 0.13	*** 0.13	*** 0.01	0.20	*** 0.11	-0.22	*** 0.07	-0.33
36	0.08	*** 0.08	0.08	-0.07	0.10	0.13	0.00	* 0.06	* 0.03	-0.28
37	0.04	0.16	0.02	0.02	-0.06	0.28	0.02	-0.18	-0.03	-0.36
13	*** 0.77	*** 0.48	*** 0.44	*** 0.80	*** 0.47	0.21	*** 0.53	0.24	*** 0.53	0.07

Contd.....

Table 62c. Correlation coefficients of significant characters of puparia from cotton population

	22	23	24	25	26	27	28	29	30	33
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										
14										
15										
16										
17										
18										
19										
20										
21										
22	1									
23	0.23	1								
24	0.14	*** 0.81	1							
25	-0.07	*** 0.43	0.54	1						
26	0.03	-0.25	*** -0.39	** -0.15	1					
27	0.15	-0.12	-0.30	* -0.48	0.42	1				
28	0.25	-0.21	-0.39	*** -0.18	* 0.37	*** 0.14	1			
29	0.14	-0.28	-0.26	-0.18	0.45	*** 0.37	* 0.50	1		
30	-0.01	0.03	-0.10	*** -0.11	*** 0.32	*** 0.26	*** 0.60	*** 0.39	1	
33	0.24	-0.30	-0.42	** -0.32	0.54	*** 0.46	*** 0.75	*** 0.62	*** 0.55	1
32	0.21	* -0.37	-0.41	-0.28	0.43	0.16	0.82	0.60	0.49	0.78
31	0.09	0.27	0.33	** 0.07	*** -0.05	0.27	0.04	0.33	* 0.19	0.08
38	* 0.40	-0.20	-0.20	-0.08	0.45	0.25	0.22	0.28	0.13	0.39
39	0.01	0.15	0.19	0.19	-0.06	-0.45	0.18	-0.26	-0.06	-0.29
34	-0.04	-0.09	0.24	0.08	-0.08	0.06	-0.13	-0.10	0.07	-0.23
35	-0.04	-0.15	0.14	*** 0.02	* -0.03	*** 0.09	*** 0.65	*** 0.51	*** 0.66	*** 0.59
36	-0.01	-0.11	-0.21	-0.26	*** 0.28	0.63	-0.17	0.23	0.18	0.25
37	-0.07	-0.12	0.22	0.00	* -0.11	*** 0.13	-0.53	*** 0.05	-0.19	-0.02
13	0.30	-0.27	-0.21	* -0.31	* -0.11	*** 0.13	*** -0.53	*** 0.05	*** -0.19	*** -0.02

Table 62d. Correlation coefficients of significant characters of puparia from cotton population

	32	31	38	39	34	35	36	37	13
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
33									
32	1								
31	0.06	1							
38	0.15	-0.10	1						
39	0.19	-0.11	-0.30	1					
34	-0.09	-0.25	0.00	0.05	1				
35	0.63	-0.01	0.20	0.05	0.94	1			
36	-0.16	-0.10	0.31	*** -0.19	0.64	0.71	1		
37	* -0.39	-0.12	* 0.36	*** -0.15	0.93	0.95	*** 0.72	1	
13	-0.39	-0.12	0.30	-0.04	0.74	*** 0.72	0.91	0.70	1

Contd.....

Table 63b. Correlation coefficients of significant characters of puparia from okra population

	11	12	14	15	16	17	18	19	20	21
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11	1									
12	*** 0.77	1								
14	*** 0.74	*** 0.98	1							
15	*** 0.69	*** 0.65	*** 0.65	1						
16	*** 0.72	*** 0.96	*** 0.97	*** 0.61	1					
17	*** 0.48	*** 0.47	*** 0.49	0.21	*** 0.53	1				
18	*** 0.71	*** 0.93	*** 0.94	*** 0.63	*** 0.97	*** 0.50	1			
19	** 0.38	** 0.37	* 0.34	*** 0.06	** 0.36	0.21	** 0.39	1		
20	*** 0.71	*** 0.92	*** 0.92	0.61	*** 0.95	*** 0.47	*** 0.98	** 0.39	1	
21	** 0.42	* 0.36	* 0.34	* 0.33	0.33	* 0.30	* 0.31	0.23	*** 0.32	1
22	*** 0.53	*** 0.66	*** 0.62	* 0.36	*** 0.67	* 0.32	*** 0.72	*** 0.53	*** 0.72	0.15
23	0.15	0.08	0.07	0.20	0.11	-0.07	0.13	0.11	* 0.15	-0.11
24	0.22	0.26	0.28	* 0.29	0.27	* -0.03	0.28	0.14	*** 0.30	-0.09
25	0.26	0.20	0.17	* 0.34	** 0.16	0.05	0.19	-0.01	0.20	-0.06
26	*** 0.65	*** 0.57	*** 0.55	*** 0.48	0.52	0.23	*** 0.56	*** 0.50	*** 0.61	** 0.45
27	0.16	* 0.31	0.23	*** 0.33	0.27	-0.06	* 0.33	0.24	0.30	0.21
28	* 0.29	* 0.34	* 0.29	* 0.34	*** 0.33	-0.14	* 0.36	* 0.28	0.40	0.28
29	* 0.32	** 0.40	** 0.42	0.13	*** 0.42	*** 0.63	** 0.43	0.20	*** 0.39	0.00
30	*** 0.50	*** 0.60	*** 0.58	*** 0.54	** 0.58	** 0.37	*** 0.58	0.19	0.59	0.12
33	** 0.40	*** 0.50	** 0.44	* 0.31	0.49	0.25	*** 0.52	** 0.41	* 0.54	-0.03
32	0.25	0.27	0.20	0.12	0.25	-0.02	0.28	* 0.31	*** 0.33	0.05
31	0.22	0.09	0.05	0.12	*** 0.05	-0.02	0.12	0.24	*** 0.17	-0.10
38	** 0.41	*** 0.47	*** 0.46	*** 0.50	0.45	-0.04	** 0.44	0.09	** 0.50	0.26
39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	** 0.00	0.00
34	0.08	-0.12	-0.12	-0.10	* -0.11	-0.02	-0.13	0.22	-0.11	-0.09
35	*** 0.63	*** 0.74	*** 0.66	*** 0.53	*** 0.70	* 0.31	*** 0.71	*** 0.46	* 0.69	* 0.31
36	* 0.30	** 0.41	*** 0.38	** 0.40	** 0.37	0.11	* 0.34	0.14	0.32	* 0.36
37	*** 0.57	*** 0.67	*** 0.62	*** 0.49	*** 0.62	* 0.34	*** 0.63	* 0.32	*** 0.62	0.27
13	*** 0.83	*** 0.76	*** 0.72	*** 0.77	*** 0.73	** 0.41	*** 0.75	** 0.38	* 0.75	** 0.42

Table 63c. Correlation coefficients of significant characters of puparia from okra population

	22	23	24	25	26	27	28	29	30	33
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										
14										
15										
16										
17										
18										
19										
20										
21										
22	1									
23	0.12	1								
24	0.19	*** 0.81	1							
25	0.13	*** 0.57	*** 0.70	1						
26	*** 0.59	0.05	0.19	0.03	1					
27	** 0.39	0.14	0.14	0.24	* 0.34	1				
28	** 0.40	0.25	* 0.29	0.24	** 0.40	*** 0.64	1			
29	0.24	-0.12	-0.07	-0.03	0.20	*** -0.06	*** -0.47	1		
30	** 0.42	-0.03	0.18	* 0.32	*** 0.52	* 0.33	0.24	* 0.32	1	
33	*** 0.52	0.05	0.15	0.03	** 0.42	* 0.23	0.15	0.26	*** 0.49	1
32	** 0.40	0.03	0.02	0.02	* 0.33	* 0.29	0.22	0.02	* 0.33	*** 0.76
31	0.20	0.17	* 0.14	0.10	** 0.38	0.22	0.18	0.06	* 0.21	*** 0.59
38	** 0.38	0.18	0.24	0.10	*** 0.55	*** 0.47	*** 0.63	-0.16	** 0.45	0.27
39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	*** 0.00
34	-0.10	0.09	* 0.07	0.05	0.16	-0.03	0.01	0.09	0.03	-0.07
35	*** 0.66	0.18	0.15	0.10	*** 0.59	*** 0.52	** 0.37	** 0.36	*** 0.53	*** 0.60
36	* 0.31	0.10	0.15	0.24	0.26	*** 0.50	*** 0.49	-0.10	0.28	0.07
37	*** 0.58	0.11	* 0.26	0.27	*** 0.56	*** 0.47	* 0.35	* 0.32	*** 0.57	** 0.45
13	*** 0.53	0.17	0.28	0.25	*** 0.56	* 0.47	** 0.35	* 0.32	*** 0.57	*** 0.45

Table 63d. Correlation coefficients of significant characters of puparia from okra population

	32	31	38	39	34	35	36	37	13
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
33									
32	1								
31	*** 0.53	1							
38	0.22	0.15	1						
39	0.00	0.00	0.20	1					
34	-0.04	0.07	0.51	0.00	1				
35	*** 0.45	** 0.37	*** 0.60	0.00	0.29	1			
36	0.08	0.01	*** 0.48	0.00	** 0.24	*** 0.83	1		
37	* 0.29	0.19	*** 0.48	0.00	* 0.30	*** 0.93	*** 0.89	1	
13	* 0.29	0.19	*** 0.20	0.00	* 0.37	*** 0.91	*** 0.79	*** 0.88	1

Table 64a. Correlation coefficients of significant characters of puparia from soybean population

	1	2	3	4	5	6	7	8	9	10
1	1									
2	-0.15	1								
3	-0.08	*** 0.61	1							
4	-0.02	*** 0.86	*** 0.58	1						
5	-0.17	0.07	0.06	0.11	1					
6	0.01	* 0.37	*** 0.50	* 0.44	0.11	1				
7	-0.03	0.16	0.19	0.19	0.06	*** 0.46	1			
8	-0.09	* 0.35	*** 0.45	* 0.40	0.15	*** 0.96	*** 0.46	1		
9	-0.21	0.30	*** 0.39	* 0.32	-0.31	0.25	0.45	0.17	1	
10	-0.06	* 0.37	*** 0.38	* 0.38	0.07	*** 0.94	* 0.38	*** 0.97	0.15	1
11	-0.30	* 0.40	* 0.48	*** 0.42	-0.15	** 0.44	0.48	* 0.39	*** 0.85	* 0.38
12	-0.03	0.34	0.39	* 0.40	0.06	*** 0.92	** 0.42	*** 0.92	0.25	*** 0.97
14	0.09	0.31	0.34	* 0.38	-0.04	*** 0.88	*** 0.44	*** 0.86	0.25	*** 0.92
15	-0.04	0.09	0.27	0.12	-0.21	0.19	0.29	0.19	*** 0.55	0.17
16	0.15	0.28	0.28	* 0.36	-0.05	*** 0.75	** 0.43	*** 0.74	0.25	*** 0.82
17	-0.26	0.24	0.26	0.17	-0.23	0.04	0.27	0.01	*** 0.58	0.05
18	0.09	0.20	0.13	0.24	0.25	*** 0.65	* 0.40	*** 0.67	0.16	*** 0.73
19	-0.10	0.21	0.34	0.19	0.04	0.00	0.38	0.01	* 0.47	-0.07
20	0.03	0.22	0.21	0.25	* 0.35	*** 0.48	0.22	*** 0.45	0.14	*** 0.55
21	-0.03	*** 0.09	-0.11	-0.13	0.24	-0.01	-0.06	0.08	0.05	0.15
22	0.18	0.31	* 0.45	* 0.40	0.19	0.33	*** 0.34	0.30	0.21	0.31
23	0.24	*** -0.05	0.22	* 0.11	-0.36	0.35	* 0.39	0.29	0.19	0.27
24	-0.17	*** 0.02	-0.29	* -0.11	0.40	-0.21	-0.09	-0.14	0.04	-0.08
25	-0.09	*** 0.18	-0.13	0.02	0.49	-0.19	-0.02	-0.09	-0.09	-0.02
26	0.03	*** 0.16	0.05	0.05	0.32	0.15	0.09	0.16	0.33	0.20
27	0.07	0.03	0.23	0.01	-0.04	*** 0.55	0.19	*** 0.52	0.27	*** 0.64
28	0.18	*** -0.03	* 0.36	0.07	* -0.51	0.28	0.09	0.18	0.22	0.11
29	0.25	*** -0.10	0.25	0.13	-0.29	0.38	0.00	0.34	0.20	0.33
30	0.19	0.07	0.36	0.12	0.28	0.03	-0.21	-0.03	-0.07	-0.02
33	-0.08	-0.22	0.03	-0.25	-0.13	0.15	-0.14	0.16	0.15	0.15
32	-0.15	0.01	0.17	-0.12	0.00	-0.04	0.03	0.01	* 0.47	-0.04
31	-0.06	-0.26	-0.25	-0.21	0.18	* -0.42	-0.04	-0.37	-0.19	* -0.40
38	* -0.41	0.32	0.26	0.17	*** -0.02	0.19	0.45	0.24	* 0.66	0.18
39	-0.32	0.00	0.10	-0.02	0.56	0.23	-0.04	0.28	-0.12	0.29
34	0.07	0.23	0.30	0.17	-0.14	-0.05	-0.14	-0.03	-0.06	0.02
35	-0.02	0.22	0.39	0.08	0.09	0.09	-0.03	0.14	-0.17	0.13
36	0.05	-0.17	0.22	-0.30	-0.17	-0.02	0.00	0.05	-0.06	0.07
37	-0.01	*** -0.11	0.16	-0.29	-0.08	-0.09	0.09	0.01	-0.08	0.04
13	-0.02	-0.22	-0.12	-0.36	0.09	-0.10	-0.02	0.00	*** 0.01	0.05

Table 64b. Correlation coefficients of significant characters of puparia from soybean population

	11	12	14	15	16	17	18	19	20	21
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11	1									
12	** 0.42	1								
14	** 0.37	*** 0.96	1							
15	*** 0.63	0.22	0.20	1						
16	* 0.39	*** 0.88	*** 0.94	0.32	1					
17	*** 0.56	0.09	0.05	0.32	0.04	1				
18	0.28	*** 0.78	*** 0.84	0.17	*** 0.90	-0.13	1			
19	*** 0.54	0.03	0.03	*** 0.58	0.12	0.09	0.27	1		
20	0.27	*** 0.62	*** 0.64	0.18	*** 0.71	0.07	*** 0.90	* 0.39	1	
21	-0.01	0.09	0.05	0.24	0.02	-0.08	0.15	0.27	0.21	1
22	* 0.30	0.33	0.35	0.30	0.34	0.06	0.17	0.12	0.16	-0.05
23	0.33	0.29	0.28	0.28	0.29	0.19	0.09	0.03	0.06	* -0.49
24	0.06	-0.19	-0.17	0.05	-0.17	-0.11	0.12	0.01	-0.03	*** 0.62
25	-0.19	-0.05	-0.11	0.01	-0.16	-0.12	0.04	0.07	0.04	*** 0.90
26	0.18	0.20	0.17	0.06	0.11	-0.11	0.25	0.10	0.14	*** 0.68
27	** 0.49	*** 0.56	*** 0.55	0.03	* 0.45	0.20	* 0.44	-0.10	0.27	0.25
28	0.26	0.12	0.12	-0.05	0.03	0.29	-0.21	-0.05	-0.12	*** -0.70
29	* 0.44	0.37	* 0.39	0.27	* 0.46	0.11	0.21	0.00	0.17	*** -0.55
30	0.05	0.11	0.01	0.37	-0.01	0.18	-0.14	0.20	0.22	0.17
33	0.27	0.10	0.05	0.16	0.04	0.08	-0.03	-0.01	-0.15	0.07
32	** 0.50	-0.09	-0.17	* 0.46	-0.14	0.18	-0.09	0.38	-0.15	* 0.37
31	-0.22	* -0.40	* -0.43	-0.16	* -0.45	0.21	-0.11	0.15	0.07	0.05
38	* 0.57	0.24	0.18	0.16	0.13	0.51	0.21	0.45	0.34	0.15
39	0.07	0.28	0.22	0.04	0.22	-0.33	0.28	0.36	0.42	0.48
34	-0.02	-0.02	-0.01	0.01	0.02	-0.10	-0.07	0.07	-0.06	0.09
35	-0.12	0.10	0.10	-0.18	0.10	-0.08	-0.14	-0.25	-0.14	0.01
36	0.03	0.02	0.01	-0.13	0.04	0.05	0.03	0.12	0.13	0.08
37	-0.06	-0.01	-0.03	-0.18	-0.02	0.01	0.00	0.04	0.06	*** 0.30
13	*** 0.07	0.00	-0.04	*** 0.07	-0.08	-0.09	0.07	*** 0.06	0.07	*** 0.80

Contd.....

Table 64c. Correlation coefficients of significant characters of puparia from soybean population

	22	23	24	25	26	27	28	29	30	33
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										
14										
15										
16										
17										
18										
19										
20										
21										
22	1									
23	** 0.39	1								
24	-0.02	* -0.55	1							
25	0.02	*** -0.65	*** 0.72	1						
26	0.17	** -0.55	*** 0.71	*** 0.74	1					
27	0.27	0.10	* 0.26	0.09	** 0.37	1				
28	0.21	*** 0.64	*** -0.71	*** -0.83	* -0.52	0.05	1			
29	* 0.38	** 0.59	* -0.51	*** -0.68	-0.33	0.11	** 0.56	1		
30	0.12	0.12	-0.18	0.12	-0.02	-0.05	0.01	0.18	1	
33	0.04	0.10	-0.16	-0.19	0.05	0.30	0.14	0.45	0.13	1
32	0.28	0.12	0.04	0.00	0.16	0.25	0.07	0.18	0.18	*** 0.74
31	-0.21	0.05	0.25	0.19	-0.07	-0.17	-0.04	*** -0.67	0.03	* -0.54
38	0.01	-0.19	-0.10	0.03	0.08	-0.06	0.02	0.04	-0.07	0.19
39	-0.12	-0.33	0.14	0.36	0.33	-0.03	-0.51	-0.33	0.24	-0.14
34	-0.20	0.19	-0.10	-0.03	-0.23	0.15	-0.01	-0.23	0.18	0.10
35	*** 0.25	* -0.04	-0.08	0.06	-0.13	0.30	0.34	0.02	-0.03	0.08
36	-0.10	0.35	-0.30	-0.32	-0.22	* 0.32	0.45	0.36	0.04	0.52
37	0.06	*** 0.28	*** -0.17	*** -0.02	*** -0.05	0.29	*** 0.17	* 0.18	0.01	0.52
13	-0.08	-0.11	** 0.32	*** 0.51	*** 0.34	0.11	-0.45	-0.28	0.09	0.26

Table 64d. Correlation coefficients of significant characters of puparia from soybean population

	32	31	38	39	34	35	36	37	13
1									
2									
3									
4									
5									
6									
7									
8									
9									
10									
11									
12									
14									
15									
16									
17									
18									
19									
20									
21									
22									
23									
24									
25									
26									
27									
28									
29									
30									
33									
32	1								
31	-0.38	1							
38	0.25	-0.11	1						
39	-0.22	-0.25	-0.10	1					
34	0.16	-0.24	-0.11	-0.13	1				
35	0.20	-0.32	-0.06	0.11	*** 0.57	1			
36	0.49	-0.05	0.25	-0.09	*** 0.46	0.57	1		
37	0.53	-0.05	0.29	-0.05	*** 0.40	0.57	0.93	1	
13	*** 0.45	0.07	0.18	0.09	0.09	0.11	0.39	*** 0.58	1

Table 65a. Correlation coefficients of significant characters of puparia from brinjal, cotton, okra and soybean populations

	1	2	3	4	5	6	7	8	9	10
1	1									
2	*** 0.10	1								
3	0.32	*** 0.70	1							
4	0.14	*** 0.93	*** 0.71	1						
5	*** 0.26	*** 0.33	0.07	*** 0.32	1					
6	*** 0.31	*** 0.46	*** 0.65	*** 0.49	-0.04	1				
7	*** 0.34	*** 0.28	*** 0.45	*** 0.25	*** -0.32	*** 0.34	1			
8	*** 0.26	*** 0.60	*** 0.78	*** 0.62	-0.03	*** 0.84	*** 0.50	1		
9	*** 0.26	*** 0.36	*** 0.53	*** 0.37	** -0.24	*** 0.37	*** 0.66	*** 0.52	1	
10	*** 0.26	*** 0.58	*** 0.75	*** 0.59	-0.06	*** 0.82	*** 0.48	*** 0.98	*** 0.51	1
11	*** 0.36	*** 0.41	*** 0.65	*** 0.41	*** -0.30	*** 0.49	*** 0.67	*** 0.63	*** 0.79	*** 0.62
12	*** 0.27	*** 0.53	*** 0.73	*** 0.56	-0.12	*** 0.78	*** 0.49	*** 0.94	*** 0.50	*** 0.97
14	*** 0.31	*** 0.51	*** 0.71	*** 0.54	-0.15	*** 0.76	*** 0.50	*** 0.91	*** 0.51	*** 0.95
15	*** 0.33	*** 0.27	*** 0.50	*** 0.28	-0.29	*** 0.39	*** 0.52	*** 0.50	*** 0.62	*** 0.49
16	*** 0.30	*** 0.51	*** 0.71	*** 0.54	-0.14	*** 0.72	*** 0.49	*** 0.87	*** 0.49	*** 0.91
17	0.12	*** 0.27	*** 0.31	** 0.25	** 0.20	* 0.16	0.12	* 0.19	* 0.17	* 0.19
18	*** 0.31	*** 0.49	*** 0.70	*** 0.50	-0.13	*** 0.68	*** 0.50	*** 0.85	*** 0.48	*** 0.87
19	0.10	* 0.17	*** 0.26	* 0.19	-0.09	0.10	0.15	0.15	*** 0.28	0.13
20	*** 0.29	*** 0.44	*** 0.68	*** 0.46	* -0.17	*** 0.60	*** 0.48	*** 0.76	*** 0.47	*** 0.79
21	0.11	* -0.19	-0.10	*** -0.26	*** -0.49	-0.11	0.12	-0.05	0.09	0.00
22	*** 0.26	*** 0.51	*** 0.63	*** 0.54	0.10	*** 0.36	** 0.25	*** 0.47	** 0.23	*** 0.47
23	-0.08	0.03	-0.07	0.02	-0.02	-0.15	* -0.18	-0.12	*** -0.27	-0.09
24	-0.01	-0.08	-0.15	-0.15	*** -0.27	* -0.19	-0.11	-0.14	** -0.21	-0.09
25	0.01	-0.15	* -0.18	** -0.22	*** -0.42	* -0.20	0.02	-0.15	-0.06	-0.09
26	*** 0.35	* 0.16	*** 0.38	0.13	*** -0.40	*** 0.26	*** 0.45	*** 0.42	*** 0.47	*** 0.43
27	*** 0.36	** 0.22	*** 0.43	** 0.19	*** -0.38	*** 0.39	*** 0.38	*** 0.46	*** 0.25	*** 0.49
28	** 0.25	*** 0.43	*** 0.52	*** 0.46	** 0.18	*** 0.37	** 0.26	*** 0.44	*** 0.28	*** 0.42
29	*** 0.35	0.11	*** 0.41	0.14	*** -0.31	*** 0.42	*** 0.45	*** 0.44	*** 0.40	*** 0.43
30	*** 0.43	* 0.17	*** 0.50	* 0.18	*** -0.41	*** 0.34	*** 0.42	*** 0.41	*** 0.33	*** 0.44
33	** 0.25	*** 0.31	*** 0.49	*** 0.31	0.04	*** 0.33	*** 0.31	*** 0.44	*** 0.29	*** 0.44
32	** 0.26	*** 0.28	*** 0.43	** 0.23	** -0.22	** 0.24	*** 0.29	*** 0.29	** 0.24	*** 0.30
31	0.15	0.06	0.08	0.03	-0.14	0.04	*** 0.26	0.07	* 0.18	0.06
38	** 0.25	*** 0.34	*** 0.50	*** 0.29	*** -0.37	*** 0.32	*** 0.45	*** 0.46	*** 0.43	*** 0.47
39	** 0.21	0.14	** 0.21	0.10	** -0.23	*** 0.27	* 0.20	*** 0.28	** 0.26	** 0.26
34	** 0.22	0.11	** 0.19	0.09	*** -0.35	0.11	0.11	0.12	0.05	* 0.17
35	-0.02	*** 0.25	*** 0.25	* 0.17	** 0.20	0.14	0.09	** 0.22	0.02	** 0.22
36	0.12	** 0.22	*** 0.34	0.13	* 0.16	** 0.23	* 0.19	*** 0.30	* 0.18	*** 0.30
37	0.04	0.11	* 0.17	0.02	* 0.16	0.06	* 0.15	0.14	0.05	* 0.15
13	0.03	** -0.20	-0.09	*** -0.28	** -0.22	-0.12	0.06	-0.06	0.02	-0.02

Table 65b. Correlation coefficients of significant characters of puparia from brinjal, cotton, okra and soybean populations

	11	12	14	15	16	17	18	19	20	21	22
1											
2											
3											
4											
5											
6											
7											
8											
9											
10											
11	1										
12	*** 0.62	1									
14	*** 0.61	*** 0.97	1								
15	*** 0.73	*** 0.50	*** 0.48	1							
16	*** 0.59	*** 0.93	*** 0.97	*** 0.51	1						
17	*** 0.30	* 0.18	0.15	** 0.20	* 0.15	1					
18	*** 0.59	*** 0.90	*** 0.93	*** 0.50	*** 0.95	0.14	1				
19	*** 0.33	0.14	0.12	*** 0.40	* 0.19	0.15	** 0.24	1			
20	*** 0.57	*** 0.82	*** 0.85	*** 0.49	*** 0.88	* 0.17	** 0.96	*** 0.27	1		
21	0.09	0.05	0.05	** 0.22	0.07	-0.11	* 0.11	** 0.27	* 0.17	1	
22	*** 0.32	*** 0.46	*** 0.46	*** 0.29	*** 0.49	** 0.22	*** 0.44	0.22	*** 0.43	-0.01	1
23	** -0.25	-0.05	-0.04	-0.13	0.01	0.01	-0.06	0.06	-0.01	*** 0.26	0.27
24	* -0.19	-0.06	-0.05	-0.09	-0.02	0.01	0.01	0.06	0.04	*** 0.58	0.13
25	-0.09	-0.06	-0.06	0.00	-0.06	-0.14	0.00	** 0.10	0.05	*** 0.91	-0.01
26	*** 0.51	*** 0.44	*** 0.45	*** 0.38	*** 0.44	0.09	*** 0.46	* 0.25	*** 0.48	*** 0.56	0.32
27	*** 0.42	*** 0.50	*** 0.50	*** 0.33	*** 0.50	0.07	*** 0.48	* 0.18	*** 0.47	*** 0.38	0.44
28	*** 0.36	*** 0.41	*** 0.39	*** 0.32	*** 0.37	* 0.18	*** 0.32	0.19	*** 0.32	-0.38	*** 0.44
29	*** 0.52	*** 0.44	*** 0.45	*** 0.37	*** 0.46	* 0.23	*** 0.44	* 0.09	*** 0.42	*** 0.01	0.19
30	*** 0.51	*** 0.47	*** 0.47	*** 0.53	*** 0.48	** 0.13	*** 0.45	** 0.21	*** 0.53	0.30	0.36
33	*** 0.37	*** 0.43	*** 0.40	*** 0.36	*** 0.42	0.16	*** 0.41	*** 0.25	*** 0.40	*** 0.06	*** 0.42
32	*** 0.39	*** 0.31	*** 0.28	*** 0.39	*** 0.31	0.02	*** 0.30	0.28	*** 0.31	0.35	0.45
31	0.13	0.04	0.04	0.07	0.03	-0.08	* 0.16	* 0.02	* 0.21	*** 0.05	*** 0.07
38	*** 0.54	*** 0.50	*** 0.50	*** 0.42	*** 0.49	0.09	*** 0.50	0.20	*** 0.53	0.27	*** 0.41
39	*** 0.29	** 0.25	** 0.24	** 0.26	** 0.22	0.09	** 0.23	0.15	** 0.23	0.07	*** 0.07
34	** 0.21	* 0.17	* 0.17	* 0.16	* 0.15	0.06	0.14	0.09	0.14	* 0.26	*** 0.14
35	0.11	* 0.19	0.15	0.00	0.11	* 0.18	0.06	-0.10	0.03	-0.19	*** 0.13
36	*** 0.29	*** 0.25	*** 0.25	0.11	*** 0.25	* 0.18	** 0.24	0.14	** 0.25	-0.09	0.07
37	0.14	0.13	0.09	0.01	0.07	* 0.20	0.10	0.04	0.09	*** 0.04	0.01
13	0.01	-0.01	-0.02	0.10	-0.03	-0.10	0.04	0.10	0.08	0.79	*** -0.03

Contd.....

Table 65c. Correlation coefficients of significant characters of puparia from brinjal, cotton, okra and soybean populations

	23	24	25	26	27	28	29	30	33	32
1										
2										
3										
4										
5										
6										
7										
8										
9										
10										
11										
12										
14										
15										
16										
17										
18										
19										
20										
21										
22										
23	1									
24	*** 0.66	1								
25	*** 0.26	*** 0.72	1							
26	0.04	*** 0.36	*** 0.57	1						
27	** 0.23	*** 0.35	*** 0.32	*** 0.57	1					
28	0.03	*** -0.29	*** -0.57	-0.06	*** 0.28	1				
29	* -0.19	-0.13	-0.09	*** 0.25	** 0.25	0.05	1			
30	0.06	0.15	** 0.23	*** 0.47	*** 0.49	** 0.24	0.42	1		
33	0.01	-0.06	-0.09	*** 0.30	*** 0.41	*** 0.43	* 0.30	*** 0.40	1	
32	0.11	0.13	* 0.17	*** 0.39	*** 0.50	*** 0.34	* 0.22	*** 0.48	*** 0.75	1
31	0.07	0.05	0.05	* 0.18	*** 0.23	0.16	** 0.12	0.16	* 0.19	* 0.19
38	0.01	0.15	* 0.19	*** 0.49	* 0.54	*** 0.27	* 0.25	*** 0.46	*** 0.34	*** 0.41
39	* -0.19	-0.09	0.02	0.13	0.13	0.02	** 0.18	** 0.24	-0.06	0.07
34	*** 0.27	*** 0.32	*** 0.32	*** 0.27	*** 0.52	0.06	** 0.17	*** 0.43	** 0.25	*** 0.45
35	-0.13	-0.09	-0.07	0.05	*** 0.28	*** 0.46	0.24	*** 0.50	*** 0.47	*** 0.44
36	-0.13	*** -0.39	*** -0.40	-0.01	*** 0.26	*** 0.44	** 0.19	0.08	*** 0.36	** 0.23
37	-0.13	*** -0.23	-0.16	0.02	* 0.20	** 0.21	*** 0.17	0.04	*** 0.34	** 0.21
13	0.11	*** 0.32	*** 0.58	*** 0.35	** 0.21	*** -0.36	*** -0.02	* 0.16	0.14	*** 0.31

Contd.....

Table 65d. Correlation coefficients of significant characters of puparia from brinjal, cotton, okra and soybean populations

	31	38	39	34	35	36	37	13
1								
2								
3								
4								
5								
6								
7								
8								
9								
10								
11								
12								
14								
15								
16								
17								
18								
19								
20								
21								
22								
23								
24								
25								
26								
27								
28								
29								
30								
33								
32								
31	1							
38	0.16	1						
39	-0.06	0.14	1					
34	0.06	*** 0.41	0.11	1				
35	-0.13	*** 0.28	0.15	*** 0.51	1			
36	0.01	*** 0.27	0.13	*** 0.38	*** 0.67	1		
37	-0.03	** 0.24	0.09	*** 0.45	*** 0.79	*** 0.86	1	
13	0.07	* 0.17	0.07	* 0.17	0.08	** 0.22	*** 0.35	1

Table 66. Correlation coefficients of significant character of adults from brinjal population

	17	18	19	20	15	16	21	22	23	24
17	1									
18	*** 0.67	1								
19	0.04	-0.11	1							
20	-0.20	-0.24	*** 0.11	1						
15	0.01	-0.01	0.00	0.01	1					
16	-0.13	-0.15	-0.11	0.18	0.20	1				
21	0.17	-0.17	0.20	0.22	*** -0.01	0.13	1			
22	0.30	-0.01	0.20	-0.08	0.05	-0.17	*** 0.80	1		
23	** -0.26	** -0.31	*** 0.35	0.15	0.13	-0.13	0.20	0.11	1	
24	-0.10	-0.10	0.26	0.18	0.16	-0.15	0.08	0.05	*** 0.72	1

Table 67. Correlation coefficients of significant character of adults from cotton population

	17	18	19	20	15	16	21	22	23	24
17	1									
18	*** 0.47	1								
19	0.34	0.08	1							
20	-0.11	0.09	0.10	1						
15	0.16	0.13	0.05	* 0.29	1					
16	* -0.10	0.07	-0.04	0.06	-0.23	1				
21	0.12	0.15	0.10	-0.16	0.04	0.57	1			
22	* 0.43	0.28	* 0.20	-0.10	* 0.10	0.27	*** 0.66	1		
23	-0.04	0.23	-0.12	-0.16	-0.07	-0.04	-0.05	-0.06	1	
24	0.12	0.25	0.08	-0.07	0.03	-0.04	0.16	0.24	*** 0.59	1

Table 68. Correlation coefficients of adults from okra population

	17	18	19	20	15	16	21	22	23	24
17	1									
18	*** 0.62	1								
19	0.41	0.26	1							
20	0.02	0.12	0.26	1						
15	0.13	0.12	0.27	0.06	1					
16	0.19	0.11	0.11	0.13	*** 0.40	1				
21	0.19	0.06	*** 0.49	0.06	*** 0.42	0.03	1			
22	0.14	0.03	*** 0.43	0.09	0.26	-0.03	*** 0.92	1		
23	0.09	0.07	* 0.31	-0.07	** 0.33	0.17	0.32	* 0.29	1	
24	* 0.32	** 0.35	* 0.32	0.03	*** 0.43	0.13	*** 0.47	*** 0.44	*** 0.47	1

Table 69. Correlation coefficients of adults from soybean population

	17	18	19	20	15	16	21	22	23	24
17	1									
18	*** 0.57	1								
19	0.23	0.04	1							
20	0.07	0.07	*** 0.41	1						
15	0.04	0.06	*** 0.38	*** 0.49	1					
16	0.33	0.32	0.08	0.21	*** 0.51	1				
21	0.24	-0.05	*** 0.51	0.24	0.26	-0.19	1			
22	0.40	0.07	*** 0.41	0.13	0.28	-0.05	*** 0.92	1		
23	0.30	0.21	0.06	0.13	-0.08	-0.05	0.07	0.06	1	
24	0.42	0.24	0.24	0.22	0.16	0.28	0.17	0.14	0.29	1

Table 70. Correlation coefficients adults from brinjal, cotton, okra and soybean population

	17	18	19	20	15	16	21	22	23	24
17	1									
18	0.52	1								
19	0.27	0.02	1							
20	-0.03	0.02	*** 0.21	1						
15	0.14	0.10	*** 0.24	*** 0.22	1					
16	0.03	0.11	0.01	0.11	*** 0.18	1				
21	*** 0.22	-0.06	*** 0.31	0.01	*** 0.18	0.21	1			
22	*** 0.35	* -0.03	*** 0.30	-0.03	*** 0.12	0.03	*** 0.80	1		
23	*** -0.02	* -0.15	*** 0.26	0.02	* 0.03	-0.04	*** 0.29	*** 0.28	1	
24	* 0.16	* 0.13	*** 0.31	0.12	*** 0.26	0.02	*** 0.30	*** 0.29	*** 0.57	1

Table 70a Correlation coefficients of significant characters of puparia and adults- details consolidated

	Adults			Puparia		
	Negative	Positive	Total	Negative	Positive	Total
Brinjal	18	27	45	53	688	741
Cotton	15	30	45	215	526	741
Okra	2	43	45	68	673	741
Soybean	5	40	45	226	515	741
All crops	7	38	45	116	625	741

Table 71. The Principal Components extracted from measurements of puparia with their eigen values and proportion of variations explained

Character No.	Eigen value	Proportion variation explained	Cumulative variation explained
1	13.748	0.4043	0.4043
2	5.3436	0.1572	0.5615
3	2.5109	0.0738	0.6354
4	1.9939	0.0586	0.6940
5	1.3359	0.0393	0.7333
6	1.0674	0.0314	0.7647
7	0.9818	0.0289	0.7936
8	0.7797	0.0229	0.8165
9	0.7042	0.0207	0.8372
10	0.6186	0.0182	0.8554
11	0.5692	0.0167	0.8721
12	0.5004	0.0147	0.8869
13	0.4659	0.0137	0.9006
14	0.4292	0.0126	0.9132
15	0.3969	0.0117	0.9249
16	0.3295	0.0097	0.9346
17	0.2758	0.0081	0.9427
18	0.2653	0.0078	0.9505
19	0.2406	0.0071	0.9575
20	0.2082	0.0061	0.9637
21	0.1947	0.0057	0.9694
22	0.1622	0.0048	0.9742
23	0.1556	0.0046	0.9787
24	0.1363	0.0040	0.9828
25	0.1286	0.0038	0.9865
26	0.1041	0.0031	0.9896
27	0.0829	0.0024	0.9920
28	0.0705	0.0021	0.9941
29	0.0658	0.0019	0.9960
30	0.0471	0.0014	0.9974
31	0.0367	0.0011	0.9985
32	0.0208	0.0006	0.9991
33	0.0178	0.0005	0.9996
34	0.0122	0.0004	1

Table 72. The first 5 Principal Components from measurements of puparia

Character No.	Prin1	Prin2	Prin3	Prin4	Prin5
1	0.12	0.07	-0.09	0.18	-0.28
2	0.14	-0.21	0.22	0.10	0.30
3	0.22	-0.12	0.07	0.10	0.08
4	0.14	-0.24	0.21	0.11	0.22
5	-0.07	-0.27	0.21	-0.02	0.32
6	0.18	-0.15	-0.003	-0.14	-0.21
7	0.17	0.02	-0.22	0.08	0.07
8	0.23	-0.14	0.01	-0.16	-0.03
9	0.17	-0.02	-0.27	0.11	0.24
10	0.23	-0.13	0.02	-0.21	-0.04
11	0.21	-0.01	-0.23	0.14	0.10
12	0.23	-0.11	0.02	-0.23	-0.07
14	0.23	-0.09	0.02	-0.25	-0.11
15	0.18	0.03	-0.19	0.11	0.16
16	0.23	-0.08	0.03	-0.24	-0.10
17	0.22	-0.06	0.02	-0.25	-0.03
19	0.22	-0.03	0.02	-0.22	-0.005
20	0.05	0.36	0.007	-0.19	0.23
22	0.15	-0.04	0.30	0.14	0.08
23	-0.01	0.17	0.43	-0.05	-0.08
24	0.003	0.282	0.31	-0.17	0.02
25	0.009	0.36	0.05	-0.20	0.24
26	0.16	0.19	-0.05	0.006	0.16
27	0.17	0.18	0.15	0.06	-0.18
28	0.12	-0.15	0.19	0.35	-0.15
29	0.14	0.02	-0.23	0.007	-0.23
30	0.17	0.13	-0.03	0.15	-0.10
31	0.15	0.03	0.13	0.24	0.05
32	0.14	0.16	0.14	0.27	0.07
38	0.18	0.12	0.02	0.10	-0.005
34	0.11	0.25	0.15	0.15	-0.31
36	0.17	0.11	0.05	0.09	-0.10
37	0.13	0.24	-0.02	-0.12	0.21
13	0.20	0.13	-0.17	0.09	0.19

Table 73a. ANOVA of Prin 1 obtained from measurements of puparia

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	723.796830	241.265610	24.00	<.0001
Error	157	1578.037266	10.051193		
Corrected Total	160	2301.834097			

Table 73b. ANOVA of Prin 2 obtained from measurements of puparia

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	609.9679904	203.3226635	121.56	<.0001
Error	157	262.5966064	1.6725898		
Corrected Total	160	872.5645968			

Table 73c. ANOVA of Prin 3 obtained from measurements of puparia

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	265.4775741	88.4925247	100.71	<.0001
Error	157	137.9574688	0.8787100		
Corrected Total	160	403.4350429			

Table 73d. ANOVA of Prin 4 obtained from measurements of puparia

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	12.7989476	4.2663159	2.07	0.1058
Error	157	322.8434918	2.0563280		
Corrected Total	160	335.6424393			

Table 73e. ANOVA of Prin 5 obtained from measurements of puparia

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	51.3944534	17.1314845	13.95	<.0001
Error	157	192.7880273	1.2279492		
Corrected Total	160	244.1824808			

Table 74. MANOVA of five principal components obtained from measurements of puparia

Statistic	Value	F Value	Num DF	Den DF	P Value
Wilks' Lambda	0.00174330	12.83	117	204.62	<.0001
Pillai's Trace	2.52533370	9.55	117	210	<.0001
Hotelling-Lawley Trace	30.11297455	17.18	117	176.56	<.0001
Roy's Greatest Root	20.85575272	37.43	39	70	<.0001

Num – Numerator; Den – Denominator and DF – Degrees of Freedom

Table 75a. Discriminant functions obtained from measurements of puparia

Character No.	Brinjal	Cotton	Okra	Soybean
Constant	-282.36942	-286.84467	-219.12620	-306.36552
1	1.11430	1.29413	1.22481	1.21065
2	-2.05671	-2.56742	-2.41976	-5.21167
3	-1.26454	-0.92932	-1.39590	-0.81126
4	2.09414	1.48322	2.26388	2.64990
5	24.14521	9.51514	14.71970	1.50877
6	0.36352	0.32734	0.34719	0.27312
7	2.36280	4.59675	3.69327	5.44841
8	-1.02745	-1.09664	-0.87473	-0.87060
9	1.12343	0.65997	2.36650	1.38059
10	0.57541	0.93998	0.60871	0.68967
11	1.81632	-1.57265	0.44265	-1.65214
12	0.07112	-0.15653	-0.01132	-0.11752
14	0.36563	0.30155	0.30021	0.15277
15	4.99369	1.28598	3.71555	0.64546
16	-0.35240	-0.39113	-0.38688	-0.22727
18	0.19994	0.42039	0.20734	0.18989
20	-0.41871	-0.54793	-0.38072	-0.32937
21	2.37612	3.63321	2.25022	5.34107
22	0.19512	1.97150	-0.03869	1.31853
23	14.50650	13.30341	10.50532	18.36979
24	8.21544	9.13436	9.53339	13.06647
25	-2.68963	-6.29454	-2.94731	-5.01485
26	2.77604	2.21563	2.34989	2.48907
27	-2.91384	-1.48876	-2.18572	-0.99249
28	5.05413	1.87575	3.41014	1.53795

Contd...

Character No.	Brinjal	Cotton	Okra	Soybean
29	0.54655	1.56469	1.54681	3.00767
30	-2.43061	2.16333	-0.56445	2.50154
31	1.00436	-4.89282	-1.62078	-6.31288
32	7.68062	11.77893	8.32328	14.50990
38	-0.31606	3.15625	0.95028	4.24435
34	20.52299	62.25537	19.82821	62.83964
36	-0.78026	0.40417	0.29826	1.59395
37	3.75871	1.96731	2.77248	1.06752
13	-6.72042	-2.97608	-5.20815	-4.98300

Table 75b. Number of observations and percent classification of puparia through Discriminant Function Analysis

Number of observations and percent classified into CROP					
From CROP	Brinjal	Cotton	Okra	Soybean	Total
Brinjal	45	0	0	0	45
	100.00	0.00	0.00	0.00	100.00
Cotton	0	35	0	1	36
	0.00	97.22	0.00	2.78	100.00
Okra	0	0	49	0	49
	0.00	0.00	100.00	0.00	100.00
Soybean	0	0	0	31	31
	0.00	0.00	0.00	100.00	100.00
Total	45	35	49	32	161
	27.95	21.74	30.43	19.88	100.00
Priors	0.25	0.25	0.25	0.25	

Table 76. The Principal Components extracted from measurements of adults with their eigen values and proportion of variations explained

	Eigen value	Difference	Proportion	Cumulative
1	3.11817200	1.76057144	0.3898	0.3898
2	1.35760056	0.35419223	0.1697	0.5595
3	1.00340834	0.11756797	0.1254	0.6849
4	0.88584037	0.16250285	0.1107	0.7956
5	0.72333752	0.24100075	0.0904	0.8860
6	0.48233677	0.14959289	0.0603	0.9463
7	0.33274388	0.23618332	0.0416	0.9879
8	0.09656056		0.0121	1.0000

Table 77. The first 3 Principal Components from measurements of adult

Character No.	Prin1	Prin2	Prin3
17	0.377547	-.358885	0.363172
18	-.049129	0.462116	0.771981
19	0.305387	0.278700	-.098274
15	0.201151	0.495126	-.008465
21	0.482580	-.174840	0.108720
22	0.495871	-.279072	0.184473
23	0.363753	0.119058	-.438211
23	0.332014	0.460653	-.156659

Table 78a. ANOVA of Prin 1 obtained from measurements of adults

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	349.68	116.56	84.35	<.0001
Error	196	270.83	1.38		
Corrected Total	199	620.51			

Table 78b. ANOVA of Prin 2 obtained from measurements of adults

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	107.60	35.86	43.25	<.0001
Error	196	162.55	0.82		
Corrected Total	199	270.16			

Table 78c. ANOVA of Prin 3 obtained from measurements of adults

Source	DF	Sum of Squares	Mean Square	F Value	P Value
Model	3	30.67	10.22	11.86	<.0001
Error	196	169.00	0.86		
Corrected Total	199	199.67			

Table 79. MANOVA of three principal components obtained from measurements of adults

Statistic	Value	F Value	Num DF	Den DF	P Value
Wilks' Lambda	0.16	57.16	9	472.3	<.0001
Pillai's Trace	1.11	38.67	9	588	<.0001
Hotelling-Lawley Trace	3.43	73.83	9	301.69	<.0001
Roy's Greatest Root	2.96	193.57	3	196	<.0001

Num – Numerator; Den – Denominator and DF – Degrees of Freedom

Table 80a. Discriminant functions obtained from measurements of adult data

Character No.	Brinjal	Cotton	Okra	Soybean
Constant	-151.43241	-184.29972	-159.92514	-136.37899
17	0.08553	2.20413	1.88597	0.13499
18	1.93432	0.20669	0.41259	2.01969
19	3.14039	2.24711	2.25392	2.79228
15	1.37792	1.25661	1.22235	1.33816
21	0.69225	0.89042	0.78521	0.66720
22	-0.35904	-0.34939	-0.38533	-0.33476
23	0.91730	1.09568	1.12339	0.73399
24	-0.73483	-0.77878	-0.90089	-0.74081

Table 80b. Number of observations and percent classification of Adult through Discriminant Function Analysis

Number of observations and percent classified into CROP					
From CROP	Brinjal	Cotton	Okra	Soybean	Total
Brinjal	35 70.00	0 0.00	0 0.00	15 30.00	50 100.00
Cotton	0 0.00	37 74.00	13 26.00	0 0.00	50 100.00
Okra	0 0.00	10 20.00	40 80.00	0 0.00	50 100.00
Soybean	5 10.00	0 0.00	0 0.00	45 90.00	50 100.00
Total	40 20.00	47 23.50	53 26.50	60 30.00	200 100.00
Priors	0.25	0.25	0.25	0.25	

Table 81. Operon primers amplifying the genomic DNA

Name of primers	Name of primers	Name of primers	Name of primers	Name of primers	Name of primers
OPA-06	OPB-03	OPC-04	OPD-03	OPE-04	OPF-02
OPA-09	OPB-04	OPC-05	OPD-05	OPE-05	OPF-12
OPA-10	OPB-05	OPC-10	OPD-06	OPE-08	OPH-09
OPA-11	OPB-08	OPC-18	OPD-07	OPE-09	OPH-16
OPA-12	OPB-09	OPC-19	OPD-08	OPE-13	
OPA-13	OPB-12		OPD-10	OPE-20	
OPA-14	OPB-19		OPD-13		
OPA-16			OPD-15		
			OPD-16		
			OPD-18		
			OPD-19		

Table 82. Operon primers not amplifying genomic DNA

Name of primers	Name of primers	Name of primers	Name of primers	Name of primers
OPA-01	OPB-01	OPC-01	OPD-01	OPE-01
OPA-02	OPB-02	OPC-02	OPD-02	OPE-02
OPA-03	OPB-06	OPC-03	OPD-04	OPE-03
OPA-04	OPB-07	OPC-06	OPD-09	OPE-06
OPA-05	OPB-10	OPC-07	OPD-11	OPE-07
OPA-07	OPB-12	OPC-08	OPD-12	OPE-10
OPA-08	OPB-13	OPC-09	OPD-13	OPE-11
OPA-15	OPB-14	OPC-11	OPD-14	OPE-12
OPA-17	OPB-15	OPC-12	OPD-20	OPE-14
OPA-18	OPB-16	OPC-13		OPE-15
OPA-19	OPB-17	OPC-14		OPE-16
OPA-20	OPB-18	OPC-15		OPE-17
	OPB-20	OPC-16		OPE-18
		OPC-17		OPE-19
		OPC-20		

Table 83. PCR products obtained with primers specifically amplifying only one population each

Primer Name	Brinjal		Primer Name	Cotton	
	No of bands	Product size in base pairs		No of bands	Product size in base pairs
A11	4	500, 750, 1000, 1250	B3	2	750, 1000
A14	2	600, 700	B9	2	600, 750
A16	3	400, 550, 750	C19	2	750, 1000
A10	3	550, 750, 2000	D3	3	500, 750, 1000
D18	1	750	B4	2	750, 1000
B19	2	750, 1000			
D7	1	1500	Primer Name	Okra	
E9	1	2500		No of bands	Product size in base pairs
D10	1	750	A12	2	500, 800
D16	1	750	B5	1	500, 750, 1250
			C4	3	750, 1250, 2000
			C18	1	750, 1000
			D19	2	700, 1000, 1500
			D5	2	750, 1000
			D6	1	1250
			D8	1	750
			E13	1	1000
			E8	3	750, 950, 1500
			E5	3	650, 800, 1500
			C10	1	750

Primer Name	Soybean	
	No of bands	Product size in base pairs
A6	4	500, 750, 950, 1000
A9	3	600, 800, 1000
B8	2	550, 800
C5	2	1000, 2000
D13	1	750, 1000
E20	1	800

Table 84. PCR products obtained with primers specifically amplifying two populations each

Primer Name	Brinjal		Cotton		Okra		Soybean	
	No of bands	Product size in base pairs	No of bands	Product size in base pairs	No of bands	Product size in base pairs	No of bands	Product size in base pairs
B12	2	500, 750					4	500, 750, 1000, 1500
E4					2	500, 750	3	500, 750, 1000
D15	1	750, 1000, 2000			1	2000		

Table 85. PCR products obtained with primers specifically amplifying three populations each

Primer Name	Brinjal		Cotton		Okra		Soybean	
	No of bands	Product size in base pairs	No of bands	Product size in base pairs	No of bands	Product size in base pairs	No of bands	Product size in base pairs
A13	2	750, 1000	3	650, 750, 1000			2	600, 700
H9	2	500, 750			3	500, 650, 850	2	500, 1000

Table 86. PCR products obtained with primers specifically amplifying all the four populations

Primer Name	Brinjal		Cotton		Okra		Soybean	
	No of bands	Product size in base pairs	No of bands	Product size in base pairs	No of bands	Product size in base pairs	No of bands	Product size in base pairs
F12	3	500, 650, 750	3	450, 750, 1250, 1500	5	450, 600, 750, 1000, 1200	5	500, 650, 750, 1000, 1250
F2	3	500, 650, 950	3	500, 650, 750	5	300, 500, 650, 750, 1000	1	500, 650, 750
H16	2	500, 950	1	400	2	400, 1000	3	750, 1000, 1250

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